

SEQUENCE LISTING

<110> A2 Biotherapeutics, Inc.
 <120> Cell Surface Receptors Responsive to Loss of Heterozygosity
 <130> A2BI-009/03W0331656-2034
 <150> 62/885,093
 <151> 2019-08-09
 <150> 63/005,670
 <151> 2020-04-06
 <160> 391
 <170> PatentIn version 3.5
 <210> 1
 <211> 45
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> CD8alpha hinge
 <400> 1

Thr	Thr	Thr	Pro	Ala	Pro	Arg	Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala
1				5					10					15	

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

Gly	Ala	Val	His	Thr	Arg	Gly	Leu	Asp	Phe	Ala	Cys	Asp
		35					40					45

<210> 2
 <211> 135
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD8alpha hinge

<400> 2
 accacgacgc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg 60
 tccctgcgcc cagaggcgtg ccggccagcg gcggggggcg cagtgcacac gagggggctg 120
 gacttcgcct gtgat 135

<210> 3
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 hinge

<400> 3

Cys	Thr	Ile	Glu	Val	Met	Tyr	Pro	Pro	Pro	Tyr	Leu	Asp	Asn	Glu	Lys
1				5					10					15	

Ser	Asn	Gly	Thr	Ile	Ile	His	Val	Lys	Gly	Lys	His	Leu	Cys	Pro	Ser
			20					25					30		

Pro	Leu	Phe	Pro	Gly	Pro	Ser	Lys	Pro
		35					40	

<210> 4
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> CD28 hinge

<400> 4

tgtaccattg aagttatgta tcctcctcct tacctagaca atgagaagag caatggaacc	60
attatccatg tgaaagggaa acacctttgt ccaagtcccc tatttcccgg accttctaag	120
ccc	123

<210> 5
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 transmembrane domain

<400> 5

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

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val
20 25

<210> 6
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> CD28 transmembrane domain

<400> 6
ttctgggtgc tggtcgttgt gggcggcgtg ctggcctgct acagcctgct ggtgacagtg 60
gccttcatca tcttttgggt g 81

<210> 7
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-2R beta transmembrane domain

<400> 7

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

Phe Ile Ile Leu Val Tyr Leu Leu Ile
20 25

<210> 8
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-2R beta transmembrane domain

<400> 8
attccgtggc tcggccacct cctcgtgggc ctcagcgggg cttttggctt catcatctta 60
gtgtacttgc tgatc 75

<210> 9
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<223> CD3 zeta activation domain

<400> 9

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

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

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

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

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

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

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

<210> 10

<211> 336

<212> DNA

<213> Artificial Sequence

<220>

<223> CD3 zeta activation domain

<400> 10

agagtgaagt tcagcaggag cgcagacgcc cccgcgtaca agcagggcca gaaccagctc 60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gcgtagaggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttac cagggactca gtacagccac caaggacacc 300

tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 11
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3 zeta activation domain

<400> 11

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

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

Asp Val Leu His Met Gln Ala Leu Pro Pro Arg
35 40

<210> 12
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3 zeta activation domain

<400> 12

agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 60

tataacgagc tcaatctagg acgaagagag gagtacgatg ttttgcacat gcaggccctg 120

ccccctcgc 129

<210> 13
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> CD28 co-stimulatory domain

<400> 13

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

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

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 14
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> CD28 co-stimulatory domain

<400> 14
aggagcaagc ggagcagact gctgcacagc gactacatga acatgacccc ccggaggcct 60
ggccccaccc ggaagcacta ccagccctac gccctccca gggatttcgc cgcctaccgg 120
agc 123

<210> 15
<211> 94
<212> PRT
<213> Artificial Sequence

<220>
<223> IL-2-Rbeta intracellular domain

<400> 15

Asn Cys Arg Asn Thr Gly Pro Trp Leu Lys Lys Val Leu Lys Cys Asn
1 5 10 15

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

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

Ser Pro Gly Gly Leu Ala Pro Glu Ile Ser Pro Leu Glu Val Leu Glu
50 55 60

Arg Asp Lys Val Thr Gln Leu Leu Pro Leu Asn Thr Asp Ala Tyr Leu
65 70 75 80

Ser Leu Gln Glu Leu Gln Gly Gln Asp Pro Thr His Leu Val
85 90

<210> 16
<211> 282
<212> DNA
<213> Artificial Sequence

<220>
<223> IL-2-Rbeta intracellular domain

<400> 16
aactgcagga acaccgggcc atggctgaag aaggtcctga agtgtaacac cccagacccc 60
tcgaagttct tttcccagct gagctcagag catggaggcg acgtccagaa gtggctctct 120
tcgcccttcc cctcatcgtc cttcagccct ggcggcctgg cacctgagat ctcgccacta 180
gaagtgctgg agaggggaaa ggtgacgcag ctgctcccc tgaacactga tgcctacttg 240
tctctccaag aactccaggg tcaggacca actcacttgg tg 282

<210> 17
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> STAT5 recruitment motif

<400> 17

Tyr Leu Ser Leu
1

<210> 18
<211> 760
<212> PRT
<213> Homo sapiens

<400> 18

Met Met Asp Gln Ala Arg Ser Ala Phe Ser Asn Leu Phe Gly Gly Glu
1 5 10 15

Pro Leu Ser Tyr Thr Arg Phe Ser Leu Ala Arg Gln Val Asp Gly Asp
20 25 30

Asn Ser His Val Glu Met Lys Leu Ala Val Asp Glu Glu Glu Asn Ala

35

40

45

Asp Asn Asn Thr Lys Ala Asn Val Thr Lys Pro Lys Arg Cys Ser Gly
 50 55 60

Ser Ile Cys Tyr Gly Thr Ile Ala Val Ile Val Phe Phe Leu Ile Gly
 65 70 75 80

Phe Met Ile Gly Tyr Leu Gly Tyr Cys Lys Gly Val Glu Pro Lys Thr
 85 90 95

Glu Cys Glu Arg Leu Ala Gly Thr Glu Ser Pro Val Arg Glu Glu Pro
 100 105 110

Gly Glu Asp Phe Pro Ala Ala Arg Arg Leu Tyr Trp Asp Asp Leu Lys
 115 120 125

Arg Lys Leu Ser Glu Lys Leu Asp Ser Thr Asp Phe Thr Ser Thr Ile
 130 135 140

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

Lys Asp Glu Asn Leu Ala Leu Tyr Val Glu Asn Gln Phe Arg Glu Phe
 165 170 175

Lys Leu Ser Lys Val Trp Arg Asp Gln His Phe Val Lys Ile Gln Val
 180 185 190

Lys Asp Ser Ala Gln Asn Ser Val Ile Ile Val Asp Lys Asn Gly Arg
 195 200 205

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

Ala Ala Thr Val Thr Gly Lys Leu Val His Ala Asn Phe Gly Thr Lys
 225 230 235 240

Lys Asp Phe Glu Asp Leu Tyr Thr Pro Val Asn Gly Ser Ile Val Ile
 245 250 255

Val Arg Ala Gly Lys Ile Thr Phe Ala Glu Lys Val Ala Asn Ala Glu
260 265 270

Ser Leu Asn Ala Ile Gly Val Leu Ile Tyr Met Asp Gln Thr Lys Phe
275 280 285

Pro Ile Val Asn Ala Glu Leu Ser Phe Phe Gly His Ala His Leu Gly
290 295 300

Thr Gly Asp Pro Tyr Thr Pro Gly Phe Pro Ser Phe Asn His Thr Gln
305 310 315 320

Phe Pro Pro Ser Arg Ser Ser Gly Leu Pro Asn Ile Pro Val Gln Thr
325 330 335

Ile Ser Arg Ala Ala Ala Glu Lys Leu Phe Gly Asn Met Glu Gly Asp
340 345 350

Cys Pro Ser Asp Trp Lys Thr Asp Ser Thr Cys Arg Met Val Thr Ser
355 360 365

Glu Ser Lys Asn Val Lys Leu Thr Val Ser Asn Val Leu Lys Glu Ile
370 375 380

Lys Ile Leu Asn Ile Phe Gly Val Ile Lys Gly Phe Val Glu Pro Asp
385 390 395 400

His Tyr Val Val Val Gly Ala Gln Arg Asp Ala Trp Gly Pro Gly Ala
405 410 415

Ala Lys Ser Gly Val Gly Thr Ala Leu Leu Leu Lys Leu Ala Gln Met
420 425 430

Phe Ser Asp Met Val Leu Lys Asp Gly Phe Gln Pro Ser Arg Ser Ile
435 440 445

Ile Phe Ala Ser Trp Ser Ala Gly Asp Phe Gly Ser Val Gly Ala Thr
450 455 460

Glu Trp Leu Glu Gly Tyr Leu Ser Ser Leu His Leu Lys Ala Phe Thr

465		470		475		480									
Tyr	Ile	Asn	Leu	Asp	Lys	Ala	Val	Leu	Gly	Thr	Ser	Asn	Phe	Lys	Val
			485						490					495	
Ser	Ala	Ser	Pro	Leu	Leu	Tyr	Thr	Leu	Ile	Glu	Lys	Thr	Met	Gln	Asn
			500					505					510		
Val	Lys	His	Pro	Val	Thr	Gly	Gln	Phe	Leu	Tyr	Gln	Asp	Ser	Asn	Trp
		515					520					525			
Ala	Ser	Lys	Val	Glu	Lys	Leu	Thr	Leu	Asp	Asn	Ala	Ala	Phe	Pro	Phe
	530					535					540				
Leu	Ala	Tyr	Ser	Gly	Ile	Pro	Ala	Val	Ser	Phe	Cys	Phe	Cys	Glu	Asp
545					550					555					560
Thr	Asp	Tyr	Pro	Tyr	Leu	Gly	Thr	Thr	Met	Asp	Thr	Tyr	Lys	Glu	Leu
				565					570					575	
Ile	Glu	Arg	Ile	Pro	Glu	Leu	Asn	Lys	Val	Ala	Arg	Ala	Ala	Ala	Glu
			580					585					590		
Val	Ala	Gly	Gln	Phe	Val	Ile	Lys	Leu	Thr	His	Asp	Val	Glu	Leu	Asn
		595					600					605			
Leu	Asp	Tyr	Glu	Arg	Tyr	Asn	Ser	Gln	Leu	Leu	Ser	Phe	Val	Arg	Asp
	610					615					620				
Leu	Asn	Gln	Tyr	Arg	Ala	Asp	Ile	Lys	Glu	Met	Gly	Leu	Ser	Leu	Gln
625					630					635					640
Trp	Leu	Tyr	Ser	Ala	Arg	Gly	Asp	Phe	Phe	Arg	Ala	Thr	Ser	Arg	Leu
				645					650					655	
Thr	Thr	Asp	Phe	Gly	Asn	Ala	Glu	Lys	Thr	Asp	Arg	Phe	Val	Met	Lys
			660					665					670		
Lys	Leu	Asn	Asp	Arg	Val	Met	Arg	Val	Glu	Tyr	His	Phe	Leu	Ser	Pro
		675					680					685			

Tyr Val Ser Pro Lys Glu Ser Pro Phe Arg His Val Phe Trp Gly Ser
690 695 700

Gly Ser His Thr Leu Pro Ala Leu Leu Glu Asn Leu Lys Leu Arg Lys
705 710 715 720

Gln Asn Asn Gly Ala Phe Asn Glu Thr Leu Phe Arg Asn Gln Leu Ala
725 730 735

Leu Ala Thr Trp Thr Ile Gln Gly Ala Ala Asn Ala Leu Ser Gly Asp
740 745 750

Val Trp Asp Ile Asp Asn Glu Phe
755 760

<210> 19
<211> 300
<212> DNA
<213> CD3 epsilon intracellular domain

<400> 19
aagaatagaa aggccaaaggc caagcctgtg acacgaggag cgggtgctgg cggcaggcaa 60
aggggacaaa acaaggagag gccaccacct gttcccaacc cagactatga gcccatccgg 120
aaaggccagc gggacctgta ttctggcctg aatcagcgca gaatcggcgg aagcaggagc 180
aagcggagca gactgctgca cagcgactac atgaacatga ccccccggag gcctggcccc 240
acccggaagc actaccagcc ctacgccct cccagggatt tcgccgccta ccggagctag 300

<210> 20
<211> 69
<212> DNA
<213> Artificial SEquence

<220>
<223> TCR beta transmembrane domain

<400> 20
accatcctct atgagatctt gctaggggaag gccaccttgt atgccgtgct ggtcagtgcc 60
ctcgtgctg 69

<210> 21
<211> 4

<212> PRT
<213> Artificial Sequence

<220>
<223> ITAM motif

<220>
<221> X
<222> (2)..(3)
<223> X can be any amino acid

<400> 21

Tyr Xaa Xaa Leu
1

<210> 22
<211> 270
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3 gamma intracellular domain

<400> 22
ggacaggatg gagttcgcca gtcgagagct tcagacaagc agactctggt gcccaatgac 60
cagctctacc agccccctcaa ggatcgagaa gatgaccagt acagccacct tcaaggaaac 120
cagttgagga ggaatggcgg aagcaggagc aagcggagca gactgctgca cagcgactac 180
atgaacatga ccccccgag gcctggcccc acccggaagc actaccagcc ctacgccct 240
cccagggatt tcgccgccta ccggagctag 270

<210> 23
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> UTY peptide

<220>
<221> X
<222> (1)..(1)
<223> X is R or G

<220>
<221> X

<222> (6)..(6)
<223> X is E or A

<220>
<221> X
<222> (8)..(8)
<223> X is V or P

<400> 23

Xaa Glu Ser Glu Glu Xaa Ser Xaa Ser Leu
1 5 10

<210> 24
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> RPSY peptide

<220>
<221> X
<222> (8)..(8)
<223> X is V or L

<400> 24

Thr Ile Arg Tyr Pro Asp Pro Xaa Ile
1 5

<210> 25
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> UTY peptide

<220>
<221> X
<222> (5)..(5)
<223> X is H or R

<220>
<221> X
<222> (7)..(7)
<223> X is D or N

<400> 25

Leu Pro His Asn Xaa Thr Xaa Leu
1 5

<210> 26
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR alpha transmembrane domain

<400> 26

Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu
1 5 10 15

Leu Met Thr Leu Arg Leu Trp
20

<210> 27
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR alpha transmembrane domain

<400> 27
gtgattgggt tccgaatcct cctcctgaaa gtggccgggt ttaatctgct catgacgctg 60
cggctgtgg 69

<210> 28
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR beta transmembrane domain

<400> 28

Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val
1 5 10 15

Leu Val Ser Ala Leu Val Leu
20

<210> 29
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3 zeta transmembrane domain

<400> 29

Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu
1 5 10 15

Thr Ala Leu Phe Leu
20

<210> 30
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3 delta intracellular domain

<400> 30

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

Leu Arg Asn Asp Gln Val Tyr Gln Pro Leu Arg Asp Arg Asp Asp Ala
20 25 30

Gln Tyr Ser His Leu Gly Gly Asn Trp Ala Arg Asn Lys Gly Gly Ser
35 40 45

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
50 55 60

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
65 70 75 80

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
85

<210> 31

<211> 269
<212> DNA
<213> Artificial Sequence

<220>
<223> CD3 delta intracellular domain

<400> 31
ggacatgaga ctggaaggct gtctggggct gccgacacac aagctctgtt gaggaatgac 60
caggtctatc agcccctccg agatcgagat gatgctcagt acagccacct tggaggaaac 120
tgggctcgga acaagggcgg aagcaggagc aagcggagca gactgctgca cagcgactac 180
atgaacatga ccccccgag gcctggcccc acccggaagc actaccagcc ctacgccctt 240
cccagggatt tcgccgccta ccggagcta 269

<210> 32
<211> 99
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3 epsilon intracellular domain

<400> 32

Lys Asn Arg Lys Ala Lys Ala Lys Pro Val Thr Arg Gly Ala Gly Ala
1 5 10 15

Gly Gly Arg Gln Arg Gly Gln Asn Lys Glu Arg Pro Pro Pro Val Pro
20 25 30

Asn Pro Asp Tyr Glu Pro Ile Arg Lys Gly Gln Arg Asp Leu Tyr Ser
35 40 45

Gly Leu Asn Gln Arg Arg Ile Gly Gly Ser Arg Ser Lys Arg Ser Arg
50 55 60

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
65 70 75 80

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
85 90 95

Tyr Arg Ser

<210> 33
<211> 89
<212> PRT
<213> Artificial Sequence

<220>
<223> CD3 gamma intracellular domain

<400> 33

Gly Gln Asp Gly Val Arg Gln Ser Arg Ala Ser Asp Lys Gln Thr Leu
1 5 10 15

Leu Pro Asn Asp Gln Leu Tyr Gln Pro Leu Lys Asp Arg Glu Asp Asp
20 25 30

Gln Tyr Ser His Leu Gln Gly Asn Gln Leu Arg Arg Asn Gly Gly Ser
35 40 45

Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr
50 55 60

Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro
65 70 75 80

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
85

<210> 34
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> SMCY peptide

<220>
<221> X
<222> (3)..(3)
<223> X is S or A

<220>
<221> X
<222> (8)..(8)

<223> X is R or Q

<400> 34

Ser Pro Xaa Val Asp Lys Ala Xaa Ala Glu Leu
1 5 10

<210> 35

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR beta intracellular domain

<400> 35

Met Ala Met Val Lys Arg Lys Asp Ser Arg
1 5 10

<210> 36

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> TCR beta intracellular domain

<400> 36

atggccatgg tcaagagaaa ggattccaga

30

<210> 37

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> CD28 intracellular domain

<400> 37

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

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

Pro Arg Asp Phe Ala Ala Tyr Arg Ser
35 40

<210> 38
<211> 123
<212> DNA
<213> Artificial Sequence

<220>
<223> CD28 intracellular domain

<400> 38
aggagcaagc ggagcagact gctgcacagc gactacatga acatgacccc ccggaggcct 60
ggccccaccc ggaagcacta ccagccctac gccctccca gggatttcgc cgcctaccgg 120
agc 123

<210> 39
<211> 42
<212> PRT
<213> Artificial Sequence

<220>
<223> 4-1BB intracellular domain

<400> 39
Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met
1 5 10 15

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

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

<210> 40
<211> 126
<212> DNA
<213> Artificial Sequence

<220>
<223> 4-1BB intracellular domain

<400> 40
aaacggggca gaaagaaact cctgtatata ttcaaacaac catttatgag gccagtacaa 60
actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120
gaactg 126

<210> 41
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 CDR-L1

<400> 41

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

<210> 42
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 CDR-L2

<400> 42

Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg
1			5					10			

<210> 43
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 CDR-L3

<400> 43

Phe	Gln	Gly	Ser	His	Val	Pro	Arg	Thr
1				5				

<210> 44
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 CDR-H1

<400> 44

Ala Ser Gly Tyr Thr Phe Thr Ser Tyr His Ile His
1 5 10

<210> 45
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 CDR-H2

<400> 45

Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly Lys

<210> 46
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 CDR-H3

<400> 46

Glu Glu Ile Thr Tyr Ala Met Asp Tyr
1 5

<210> 47
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 CDR-L1

<400> 47

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

<210> 48
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> HLA-A*02 CDR-L2

<400> 48

Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg
1 5 10

<210> 49

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> HLA-A*02 CDR-L3

<400> 49

Met Gln Gly Ser His Val Pro Arg Thr
1 5

<210> 50

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> HLA-A*02 CDR-H1

<400> 50

Ser Gly Tyr Thr Phe Thr Ser Tyr His Met His
1 5 10

<210> 51

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> HLA-A*02 CDR-H2

<400> 51

Trp Ile Tyr Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> 52
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 CDR-H3

<400> 52

Glu Gly Thr Tyr Tyr Ala Met Asp Tyr
1 5

<210> 53
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 ScFv

<400> 53

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

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

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Ser His Val Pro Arg Thr Ser Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly
130 135 140

Ala Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
145 150 155 160

Tyr His Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp
165 170 175

Ile Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys
180 185 190

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
195 200 205

Tyr Met His Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
210 215 220

Cys Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
225 230 235 240

Thr Ser Val Thr Val Ser Ser
245

<210> 54
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 ScFv

<400> 54

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe
50 55 60

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

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

Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

Gly Gly Gly Gly Ser Gly Gly Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ser
145 150 155 160

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Lys Val Ser
180 185 190

Asn Arg Phe Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
210 215 220

Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 55
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 ScFv

<400> 55

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe
50 55 60

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

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

Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

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

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

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
165 170 175

Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser
180 185 190

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

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

Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 56
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 ScFv

<400> 56

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

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

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

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe
50 55 60

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

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

Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

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

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

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
165 170 175

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

Asn Arg Phe Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

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

Thr Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 57
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 ScFv

<400> 57

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Trp Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe
50 55 60

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

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

Ala Arg Glu Glu Ile Thr Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110

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

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

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

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
165 170 175

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

Asn Arg Phe Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

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

Thr Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Val Glu Val Lys
245

<210> 58
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 ScFv

<400> 58

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Tyr Ile Tyr Pro Gly Asn Val Asn Thr Glu Tyr Asn Glu Lys Phe
50 55 60

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

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

Ala Arg Glu Glu Ile Thr Tyr Ala Met 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 Gly Gly Asp Val Gln Met Thr Gln Ser Pro Ser
130 135 140

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

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Met Glu Trp Tyr
165 170 175

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

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

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

Thr Tyr Tyr Cys His Gln Gly Ser His Val Pro Arg Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Val Glu Val Lys
245

<210> 59
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 ScFv

<400> 59

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

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe
50 55 60

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

Met Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Phe Cys
85 90 95

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

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

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

Ser Leu Pro Val Ser Leu Gly Asp Gln Val Ser Ile Ser Cys Arg Ser
145 150 155 160

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
165 170 175

Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
180 185 190

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

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

Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys
245

<210> 60

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> HLA-A*02 ScFv

<400> 60

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe
50 55 60

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

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

Ala Arg Glu Gly Thr Tyr Tyr Ala Met Asp Tyr Trp Gly Lys Gly Ser
100 105 110

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

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

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

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
165 170 175

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

Asn Arg Phe Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

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

Thr Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Pro
225 230 235 240

Gly Thr Lys Val Asp Ile Lys
245

<210> 61
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 ScFv

<400> 61

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe
50 55 60

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

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

Ala Arg Glu Gly Thr Tyr Tyr Ala Met 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 Gly Gly Asp Ile Gln Met Thr Gln Ser Pro Ser
130 135 140

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

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
165 170 175

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

Asn Arg Phe Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

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

Thr Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gln
225 230 235 240

Gly Thr Lys Val Glu Val Lys
245

<210> 62
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 ScFv

<400> 62

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe
50 55 60

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

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

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

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

Gly Gly Gly Gly Ser Gly Gly Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ser
145 150 155 160

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Lys Val Ser
180 185 190

Asn Arg Phe Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
210 215 220

Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 63
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 ScFv

<400> 63

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

Ser Val Lys Val Ser Cys Thr Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

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

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

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

Ala Arg Glu Gly Thr Tyr Tyr Ala Met Asp Leu 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 Gly Gly Glu Ile Val Leu Thr Gln Ser Pro Gly
130 135 140

Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ser
145 150 155 160

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Ala Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Ser Lys Val Ser
180 185 190

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala
210 215 220

Val Tyr Tyr Cys Gln Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 64
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> HLA-A*02 ScFv

<400> 64

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

Gly Trp Ile Tyr Pro Gly Asp Gly Ser Thr Gln Tyr Asn Glu Lys Phe
50 55 60

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

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

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

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

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

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

Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Asp Trp Tyr
165 170 175

Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser
180 185 190

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

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

Val Tyr Tyr Cys Met Gln Gly Ser His Val Pro Arg Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 65

<211> 670

<212> PRT

<213> Homo sapiens

<400> 65

Met Thr Pro Ile Leu Thr Val Leu Ile Cys Leu Gly Leu Ser Leu Gly
1 5 10 15

Pro Arg Thr His Val Gln Ala Gly His Leu Pro Lys Pro Thr Leu Trp
20 25 30

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

Cys Gln Gly Gly Gln Glu Thr Gln Glu Tyr Arg Leu Tyr Arg Glu Lys
50 55 60

Lys Thr Ala Leu Trp Ile Thr Arg Ile Pro Gln Glu Leu Val Lys Lys
65 70 75 80

Gly Gln Phe Pro Ile Pro Ser Ile Thr Trp Glu His Ala Gly Arg Tyr
85 90 95

Arg Cys Tyr Tyr Gly Ser Asp Thr Ala Gly Arg Ser Glu Ser Ser Asp
100 105 110

Pro Leu Glu Leu Val Val Thr Gly Ala Tyr Ile Lys Pro Thr Leu Ser
115 120 125

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

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

Glu Asp Glu His Pro Gln Cys Leu Asn Ser Gln Pro His Ala Arg Gly
165 170 175

Ser Ser Arg Ala Ile Phe Ser Val Gly Pro Val Ser Pro Ser Arg Arg
180 185 190

Trp Trp Tyr Arg Cys Tyr Ala Tyr Asp Ser Asn Ser Pro Tyr Glu Trp
195 200 205

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

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

Thr Leu Thr Leu Gln Cys Gly Ser Asp Ala Gly Tyr Asn Arg Phe Val

245

250

255

Leu Tyr Lys Asp Gly Glu Arg Asp Phe Leu Gln Leu Ala Gly Ala Gln
 260 265 270

Pro Gln Ala Gly Leu Ser Gln Ala Asn Phe Thr Leu Gly Pro Val Ser
 275 280 285

Arg Ser Tyr Gly Gly Gln Tyr Arg Cys Tyr Gly Ala His Asn Leu Ser
 290 295 300

Ser Glu Trp Ser Ala Pro Ser Asp Pro Leu Asp Ile Leu Ile Ala Gly
 305 310 315 320

Gln Phe Tyr Asp Arg Val Ser Leu Ser Val Gln Pro Gly Pro Thr Val
 325 330 335

Ala Ser Gly Glu Asn Val Thr Leu Leu Cys Gln Ser Gln Gly Trp Met
 340 345 350

Gln Thr Phe Leu Leu Thr Lys Glu Gly Ala Ala Asp Asp Pro Trp Arg
 355 360 365

Leu Arg Ser Thr Tyr Gln Ser Gln Lys Tyr Gln Ala Glu Phe Pro Met
 370 375 380

Gly Pro Val Thr Ser Ala His Ala Gly Thr Tyr Arg Cys Tyr Gly Ser
 385 390 395 400

Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp Pro Leu Glu
 405 410 415

Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly
 420 425 430

Pro Thr Ser Thr Ser 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 Ile 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 His Thr Gln Pro Glu Asp Gly
530 535 540

Val Glu Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val
545 550 555 560

Thr Tyr Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser
565 570 575

Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln
580 585 590

Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala
595 600 605

Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg
610 615 620

Glu Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val
625 630 635 640

Pro Ser Ile Tyr Ala Thr Leu Ala Ile His Pro Ser Gln Glu Gly Pro
645 650 655

Ser Pro Ala Val Pro Ser Ile Tyr Ala Thr Leu Ala Ile His
660 665 670

<211> 3229
<212> DNA
<213> Homo sapiens

<400> 66

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tgggccctcc tggaggtggt tagaccttcc gagagagaaa ctgagacaca tgagagggaa	120
gaaatgactc agtggtgaga ccctgtggag tcccaccac aaccagcaca ctgtgaccca	180
ctgcacaaac ctctagccca cagctcactt cctcctttaa gaagagaaga gaaaagagga	240
gaggagagga ggaacagaaa agaaaagaaa agaaaaagtg ggaaacaaat aatctaagaa	300
tgaggagaaa gcaagaagag tgacccccctt gtgggcactc cattggtttt atggcgcctc	360
tactttctgg agtttgtgta aaacaaaaat attatggtct ttgtgcacat ttacatcaag	420
ctcagcctgg gcggcacagc cagatgcgag atgcgtctct gctgatctga gtctgcctgc	480
agcatggacc tgggtcttcc ctgaagcatc tccagggtct gagggacgac tgccatgcac	540
cgagggtca tccatccaca gagcagggca gtgggaggag acgcatgac cccatcctc	600
acggtcctga tctgtctcgg gctgagtctg ggccccgga cccacgtgca ggcagggcac	660
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ggccgctcag agagcagtga cccctggag ctggtggtga caggagccta catcaaacc	960
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gactcacagg tggcatttga tggcttcatt ctgtgtaagg aaggagaaga tgaacacca	1080
caatgcctga actcccagcc catgcccgt gggtcgtccc gcgccatctt ctccgtgggc	1140
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tatgagtgggt ctctaccag tgatctcctg gagctcctgg tcctaggtgt ttctaagaag	1260
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tgtggctctg atgctggcta caacagattt gttctgtata aggacgggga acgtgacttc	1380
cttcagctcg ctggcgaca gccccaggct gggctctccc aggccaaactt caccctgggc	1440
cctgtgagcc gtcctacgg gggccagtac agatgctacg gtgcacacaa cctctcctcc	1500

gagtggtcgg cccccagcga ccccctggac atcctgatcg caggacagtt ctatgacaga	1560
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tgtcagtcac agggatggat gcaaactttc cttctgacca aggagggggc agctgatgac	1680
ccatggcgtc taagatcaac gtaccaatct caaaaatacc aggctgaatt ccccatgggt	1740
cctgtgacct cagcccatgc ggggacctac aggtgctacg gctcacagag ctccaaacct	1800
tacctgctga ctcacccag tgacccctg gagctcgtgg tctcaggacc gtctgggggc	1860
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cccaccgggt cggatcccca gagtggcttg ggaaggcacc tgggggttgt gatcggcatc	1980
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gatgcccagg aagaaaacct ctatgctgcc gtgaagcaca cacagcctga ggatggggtg	2220
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gtttcagtga gccaaagatcg caccactgct ctccagcctg gcgacagagg gagactccat 3180

ctcaaattaa aaaaaaaaaa aaaaaagaaa gaaaaaaaaa aaaaaaaaaa 3229

<210> 67
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> ITIM

<400> 67

Asn Leu Tyr Ala Ala Val
1 5

<210> 68
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> ITIM

<400> 68

Val Thr Tyr Ala Glu Val
1 5

<210> 69
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> ITIM

<400> 69

Val Thr Tyr Ala Gln Leu
1 5

<210> 70
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> ITIM

<400> 70

Ser Ile Tyr Ala Thr Leu
1 5

<210> 71

<211> 35

<212> PRT

<213> Artificial Sequence

<220>

<223> ITIM 1-2

<400> 71

Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly Val Glu
1 5 10 15

Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr
20 25 30

Ala Glu Val
35

<210> 72

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> ITIM 2-3

<400> 72

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

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

Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu
35 40 45

Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu
50 55

<210> 73
<211> 36
<212> PRT
<213> Artificial Sequence

<220>
<223> ITIM 3-4

<400> 73

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

Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro Ser Ile
20 25 30

Tyr Ala Thr Leu
35

<210> 74
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> ITIM 1-3

<400> 74

Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly Val Glu
1 5 10 15

Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr
20 25 30

Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro
35 40 45

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

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

Asp Val Thr Tyr Ala Gln Leu
85

<210> 75
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
<223> ITIM 2-4

<400> 75

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

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

Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu
35 40 45

Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg
50 55 60

Arg Glu Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala
65 70 75 80

Val Pro Ser Ile Tyr Ala Thr Leu
85

<210> 76
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> ITIM 1-4

<400> 76

Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly Val Glu
1 5 10 15

Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr
20 25 30

Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro
35 40 45

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

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

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

Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro Ser
100 105 110

Ile Tyr Ala Thr Leu
115

<210> 77
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> D3D4 domain

<400> 77

Tyr Gly Ser Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp
1 5 10 15

Pro Leu Glu Leu
20

<210> 78
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> short hinge

<400> 78

Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly Pro
1 5 10 15

Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser
20 25 30

Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly
35 40

<210> 79
<211> 86
<212> PRT
<213> Artificial Sequence

<220>
<223> hinge- transmembrane

<400> 79

Tyr Gly Ser Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp
1 5 10 15

Pro Leu Glu Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro
20 25 30

Thr Thr Gly Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr
35 40 45

Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val
50 55 60

Val Ile Gly Ile Leu Val Ala Val Ile Leu Leu Leu Leu Leu Leu
65 70 75 80

Leu Leu Phe Leu Ile Leu
85

<210> 80
<211> 190
<212> PRT
<213> Artificial Sequence

<220>
<223> hinge-transmembrane-intracellular domain

<400> 80

Val Val Ile Gly Ile Leu Val Ala Val Ile Leu Leu Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Phe Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp
20 25 30

Thr Ser Thr Gln Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val
35 40 45

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

Ala Asp Ala Gln Glu Glu Asn Leu Tyr Ala Ala Val Lys His Thr Gln
65 70 75 80

Pro Glu Asp Gly Val Glu Met Asp Thr Arg Ser Pro His Asp Glu Asp
85 90 95

Pro Gln Ala Val Thr Tyr Ala Glu Val Lys His Ser Arg Pro Arg Arg
100 105 110

Glu Met Ala Ser Pro Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr
115 120 125

Lys Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala
130 135 140

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

Thr Leu Arg Arg Glu Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro
165 170 175

Ser Pro Ala Val Pro Ser Ile Tyr Ala Thr Leu Ala Ile His
180 185 190

<210> 81

<211> 167

<212> PRT

<213> Artificial Sequence

<220>

<223> LILRB1 intracellular domain

<400> 81

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

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

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

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

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

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

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

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

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

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

Tyr Ala Thr Leu Ala Ile His
165

<210> 82

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> LILRB1 hinge-transmembrane-intracellular domain

<400> 82

Tyr Gly Ser Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp
1 5 10 15

Pro Leu Glu Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro
20 25 30

Thr Thr Gly Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr
35 40 45

Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val
50 55 60

Val Ile Gly Ile Leu Val Ala Val Ile Leu Leu Leu Leu Leu Leu
65 70 75 80

Leu Leu Phe Leu Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr
85 90 95

Ser Thr Gln Arg Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly
100 105 110

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

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

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

Gln Ala Val Thr Tyr Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu
165 170 175

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

Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala
195 200 205

Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr
210 215 220

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

Pro Ala Val Pro Ser Ile Tyr Ala Thr Leu Ala Ile His
245 250

<210> 83
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> LILRB1 hinge-TM-intracellular domain

<400> 83

Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro Thr Thr Gly Pro
1 5 10 15

Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr Pro Thr Gly Ser
20 25 30

Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly Val Val Ile Gly Ile
35 40 45

Leu Val Ala Val Ile Leu Leu Leu Leu Leu Leu Leu Leu Phe Leu
50 55 60

Ile Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln Arg
65 70 75 80

Lys Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro Thr
85 90 95

Asp Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln Glu
100 105 110

Glu Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly Val
115 120 125

Glu Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr
130 135 140

Tyr Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro
145 150 155 160

Pro Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala
165 170 175

Glu Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro
180 185 190

Gln Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Glu
195 200 205

Ala Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro
210 215 220

Ser Ile Tyr Ala Thr Leu Ala Ile His
225 230

<210> 84
<211> 63
<212> PRT
<213> Artificial Sequence

<220>
<223> LILRB1 hinge domain

<400> 84

Tyr Gly Ser Gln Ser Ser Lys Pro Tyr Leu Leu Thr His Pro Ser Asp
1 5 10 15

Pro Leu Glu Leu Val Val Ser Gly Pro Ser Gly Gly Pro Ser Ser Pro
20 25 30

Thr Thr Gly Pro Thr Ser Thr Ser Gly Pro Glu Asp Gln Pro Leu Thr
35 40 45

Pro Thr Gly Ser Asp Pro Gln Ser Gly Leu Gly Arg His Leu Gly
50 55 60

<210> 85
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> LILRB1 transmembrane domain

<400> 85

Val Val Ile Gly Ile Leu Val Ala Val Ile Leu Leu Leu Leu Leu Leu
1 5 10 15

Leu Leu Leu Phe Leu Ile Leu
20

<210> 86
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN binding domain

<400> 86

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

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

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

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

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Asp Ile Val Met Thr Gln Ser Ser Ser Leu Ser Ala
130 135 140

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

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

Leu Leu Ile Tyr Thr Ala Ser Ile Leu Gln Asn Gly Val Pro Ser Arg
180 185 190

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
195 200 205

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

Thr Pro Asp Phe Gly Pro Gly Thr Lys Val Glu Ile Lys
225 230 235

<210> 87
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN binding domain

<400> 87
caggtgcagc tgggtgcagtc tggggctgag gtggagaagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggata caccttcacc gactactata tgcactgggt gcgacaggcc 120
cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtgggtg cacaactat 180
gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccatcag cacagcctac 240

atggagctga gcaggctgag atctgacgac acggccgtgt attactgtgc gtctggctgg 300
 gactttgact actggggcca gggaaccctg gtcaccgtgt cctcaggcgg aggtggaagc 360
 ggagggggag gatctggcgg cggaggaagc ggaggcgaca tcgtgatgac ccagtcttcc 420
 tccctgtctg catctgtcgg agacagagtc accatcactt gccgggccag tcagagcatt 480
 aggtactatt taagttggta tcagcagaaa ccaggaaaag cccctaagct cctgatctat 540
 actgcatcca ttttacaaaa tgggggtccca tcaaggttca gtggcagtgg atctgggaca 600
 gatttcactc tcaccatcag cagcctgcaa cctgaggatt ttgcaactta ttactgcctc 660
 cagacttaca ctactccgga ctttggccca gggaccaagg tggaatcaa a 711

<210> 88
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MSLN binding domain

<400> 88

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Thr Phe Arg Gly Tyr
 20 25 30

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

Gly Ile Ile Asn Pro Ser Gly Gly Ser Arg Ala Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

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

Ala Arg Thr Ala Ser Cys Gly Gly Asp Cys Tyr Tyr Leu Asp Tyr Trp
 100 105 110

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

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

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

Thr Cys Arg Ala Ser Glu Asn Val Asn Ile Trp Leu Ala Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Ser Ser Ser
180 185 190

Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Ala
195 200 205

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

Tyr Tyr Cys Gln Gln Tyr Gln Ser Tyr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 89
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN binding domain

<400> 89
caggtgcagc tgggtgcagtc tggggctgag gtgagggcac ctggggcctc agtgaagatt 60
tcctgcaagg cttctggatt caccttcaga ggctactata tccactgggt gcgacaggcc 120
cctggacaag ggcttgagt gatgggaatc atcaacccta gtggtggtag cagagcctac 180
gcacagaagt tccagggcag ggtcaccatg accagggaca cttccacgag cacagtctac 240

atggagctga gcagcctgag atctgacgac acggccatgt attactgtgc gagaaccgca 300
 agttgtggtg gtgactgcta ctaccttgac tactggggcc agggaaccct ggtcaccgtg 360
 tcctcaggcg gaggtggaag cggaggggga ggatctggcg gcggaggaag cggaggcgac 420
 atccagatga cccagtctcc tcccaccctg tctgcatctg taggagacag agtcaccatc 480
 acttgccggg ccagtgagaa tgttaatatc tggttggcct ggtatcagca gaaaccaggg 540
 aaagccccta agctcctgat ctataagtca tccagtttag caagtggggt cccatcaagg 600
 ttcagtggca gtggatctgg ggcagaattc actctcacca tcagcagcct gcagcctgat 660
 gatTTTgcaa cttattactg ccaacagtat caaagttacc ccctcacttt cggcggaggg 720
 accaaggtgg aaatcaaa 738

<210> 90
 <211> 242
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MSLN binding domain

<400> 90

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
 20 25 30

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

Gly Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser Tyr Asn Gln Lys Phe
 50 55 60

Arg Gly Arg Val Thr Ile Thr Arg Asp Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80

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

Ala Arg Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr Trp Gly Gln Gly
100 105 110

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

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

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

Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly
165 170 175

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

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

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

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

Ile Lys

<210> 91
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN binding domain

<400> 91
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60
tcctgcaagg cttctggata ctcattcacc ggctacacca tgaactgggt gaggcaggcc 120
cctggacaaa gacttgagtg gatgggactt atcaccctt acaatggtgc ttctagctac 180

aaccagaagt tcaggggcag ggtcacaatc actagagaca cgtcagccag cacagcctac 240
atggagctct ccagcctgag atctgaagac actgcagtct attactgtgc aaggggggggt 300
tacgacggga ggggttttga ctactggggc cagggaacca cggtcaccgt gtcctcaggc 360
ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcga catccagatg 420
accagttctc cttcaagctt gtctgcatct gtaggagaca gggtcaccat cacttgcagt 480
gccagctcaa gtgtaagtta catgcactgg tatcagcaga aaccaggcaa ggcccctaag 540
agattgatct atgacacatc caaattagca agtgggggtcc caagtcgctt cagtggcagt 600
ggatctggga ccgaattcac tctcaccatc agcagcttgc agcctgagga ttttgcaact 660
tattactgcc agcagtggag tggttaccct ctcacgttcg gtcagggggac aaagttggaa 720
atcaaa 726

<210> 92
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> MSLN binding domain

<400> 92

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
20 25 30

Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
35 40 45

Gly Leu Ile Thr Pro Tyr Asn Gly Ala Ser Ser Tyr Asn Gln Lys Phe
50 55 60

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

Met Asp Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Gly Gly Tyr Asp Gly Arg Gly Phe Asp Tyr Trp Gly Gln Gly
100 105 110

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

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

Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser
145 150 155 160

Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly
165 170 175

Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly
180 185 190

Val Pro Gly Arg Phe Ser Gly Ser Gly Ser Gly Asn Ser Tyr Ser Leu
195 200 205

Thr Ile Ser Ser Val Glu Ala Glu Asp Asp Ala Thr Tyr Tyr Cys Gln
210 215 220

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

Ile Lys

<210> 93
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> MSLN binding domain

<400> 93
caggtgcagc tgcagcagtc tgggcctgag ctggagaagc ctggggcctc agtgaagatt 60
tcctgcaagg cttctggata ctcattcacc ggctacacca tgaactgggt gaagcagagc 120

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

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Glu Asn Val Leu Thr Gln Ser
130 135 140

Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys
145 150 155 160

Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro
165 170 175

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

Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser
195 200 205

Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys
210 215 220

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

Glu Leu Lys

<210> 95
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<223> CEA binding domain

<400> 95
caggtccagc tgcagcagtc tggggcagag cttgtgaggt cagggacctc agtcaagttg

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

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Glu Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Leu Ala Pro Arg Leu Leu Ile Tyr Ser Thr Ser Asn Leu Ala Ser
180 185 190

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys
210 215 220

Gln Gln Arg Ser Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys

<210> 97

<211> 729

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA binding domain

<400> 97
caggtccagc tggtgcagtc tggggcagag gtgaagaaac caggggcctc agtcaaggtg 60
tcctgcaaag cttctggctt caacattaaa gactcctata tgcactgggt gaggcaggcg 120
cctggacagg gcctggagtg gatgggatgg attgatacctg agaatgggtga tactgaatat 180
gccccgaagt tccagggcag ggtcactatg actacagaca catccacctc cacagcctac 240
atggagctca ggagcctgag atctgacgac actgccgtct attactgtaa tgaagggaca 300
ccgacagggc catactatatt tgactactgg ggtcaaggaa ccacagtcac cgtgtcctca 360
ggcggaggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgagatcggtt 420
ctcaccagct ctccagcaac cttgtctctg tctccagggg agagggccac cctaagctgc 480
agtgccagct caagtgtaag ttacatgcac tggtaccagc agaagccagg ctttgctccc 540
agactcctga tttatagcac atccaacctg gcttctggaa tccctgatcg cttcagtggc 600
agtggatctg ggaccgattt cactctcaca atcagccgac tggagcctga agatttcgcc 660
gtttattact gccagcaaag gagtagttac ccgctcacgt tcggtcaggg gaccaagctg 720
gagatcaaa 729

<210> 98
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA binding domain

<400> 98

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

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

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

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

Leu Arg Ser Ser Tyr Ala Ser Trp Tyr Arg Gln Arg Pro Gly Gln Ala
165 170 175

Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro
180 185 190

Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile
195 200 205

Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Trp Asn Ser Ser
210 215 220

Tyr Ala Trp Leu Pro Tyr Val Val Phe Gly Gly Gly Thr Lys Leu Thr
225 230 235 240

Val Leu Gly

<210> 99

<211> 729

<212> DNA

<213> Artificial Sequence

<220>

<223> CEA binding domain

<400> 99

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gaggtgcagc tggcggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc      60
tcctgtgcag cctctggatt cacctttagc agcgatgcca tgagctgggt ccgccaggct      120
ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgag agccgaggac acggccgtgt attactgtgc aaagtctaata      300
gagtttcttt ttgactactg gggccaaggt accctgggtca ccgtgtcgag tggcggaggt      360
ggaagcggag ggggaggatc tggcggcgga ggaagcggag gctcttctga gctgactcag      420
gaccctgctg tgtctgtggc cttgggacag acagtcagga tcacatgcca aggagacagc      480
ctcagaagct cttatgcaag ctggtaccgg cagaggccag gacaggcccc tgtacttgtc      540
atctatggta aaaacaaccg gccctcaggg atcccagacc gattctcttg ctccagctca      600
ggaaacacag cttccttgac catcactggg gctcaggcgg aagatgaggc tgactattac      660
tggaactcca gctacgcttg gctgccctac gtggtattcg gcggaggggac caagctgacc      720
gtcctaggt                                         729
```

<210> 100

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> CEA binding domain

<400> 100

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

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

```
Tyr Met His Trp Leu Arg Gln Gly Pro Gly Gln Arg Leu Glu Trp Ile
35              40              45
```

```
Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
50              55              60
```

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

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

Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Glu Asn Val Leu Thr Gln Ser
130 135 140

Pro Ser Ser Met Ser Val Ser Val Gly Asp Arg Val Asn Ile Ala Cys
145 150 155 160

Ser Ala Ser Ser Ser Val Pro Tyr Met His Trp Leu Gln Gln Lys Pro
165 170 175

Gly Lys Ser Pro Lys Leu Leu Ile Tyr Leu Thr Ser Asn Leu Ala Ser
180 185 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser
195 200 205

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

Gln Gln Arg Ser Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys

<210> 101
<211> 729
<212> DNA
<213> Artificial Sequence

<220>

<223> CEA binding domain

<400> 101

```
cagggtccagc tggagcagtc tggggcaggg gttgtgaagc caggggcctc agtcaagttg      60
tcctgcaaag cttctggctt caacattaaa gactcctata tgcactggtt gaggcagggg      120
cctggacagc gcctggagtg gattggatgg attgatacctg agaatggtga tactgaatat      180
gccccgaagt tccagggcaa ggccactttt actacagaca catccgcaa cacagcctac      240
ctgggggtca gcagcctgag acctgaggac actgccgtct attactgtaa tgaagggaca      300
ccgacagggc catactattt tgactactgg ggtcaaggaa ccctagtcac cgtgtcctca      360
ggcgggagtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgagaacgtt      420
ctcaccagct ctccaagctc tatgtctgta tctgtcgggg acagggtcaa catcgcctgc      480
agtgccagct caagtgtacc ttacatgcac tggctccagc agaagccagg caaatctccc      540
aaactcctga tttatctcac atccaacctg gcttctggag tccctagccg cttcagtggc      600
agtggatctg ggaccgatta ctctctcaca atcagctcag tgcagcctga agatgctgcc      660
acttattact gccagcaaag gagtagttac ccgctcacgt tcggtggtgg gaccaagctg      720
gagatcaaa                                     729
```

<210> 102

<211> 249

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR ScFv

<400> 102

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

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

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

Ala Val Ile Trp Asp Asp Gly Ser Tyr Lys Tyr Tyr Gly 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 Asp Gly Ile Thr Met Val Arg Gly Val Met Lys Asp Tyr Phe
100 105 110

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Ala Ile
130 135 140

Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
145 150 155 160

Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Ala Leu Val
165 170 175

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
180 185 190

Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Glu
195 200 205

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
210 215 220

Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Leu Thr Phe
225 230 235 240

Gly Gly Gly Thr Lys Val Glu Ile Lys
245

<210> 103

<211> 747

<212> DNA
<213> Artificial Sequence

<220>
<223> EGFR ScFv

<400> 103
caggtgcagc tgggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60
tcctgtgcag cgtctggatt caccttcagt acctatggca tgcactgggt ccgccaggct 120
ccaggcaagg ggctggagtg ggtggcagtt atatgggatg atggaagtta taaatactat 180
ggagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
ctgcaaatac acagcctgag agccgaggac acggctgtgt attactgtgc gagagatggt 300
attactatgg ttcggggagt tatgaaggac tactttgact actggggcca gggaaccctg 360
gtcaccgtct cctcaggcgg aggtggaagc ggagggggag gatctggcgg cggaggaagc 420
ggaggcgcca tccagttgac ccagtctcca tcctccctgt ctgcatctgt aggagacaga 480
gtcaccatca cttgccgggc aagtcaggac attagcagtg ctttagtctg gtatcagcag 540
aaaccaggga aagctcctaa gtcctgatc tatgatgcct ccagtttgga aagtggggtc 600
ccatcaaggt tcagcggcag tgaatctggg acagatttca ctctcaccat cagcagcctg 660
cagcctgaag attttgcaac ttattactgt caacagttta atagttaccg gtcactttc 720
ggcggaggga ccaaggtgga gatcaaa 747

<210> 104
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR ScFv

<400> 104

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

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

Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu
130 135 140

Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Gly Met His Trp
145 150 155 160

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Trp
165 170 175

Asp Asp Gly Ser Tyr Lys Tyr Tyr Gly Asp Ser Val Lys Gly Arg Phe
180 185 190

Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn
195 200 205

Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Gly
210 215 220

Ile Thr Met Val Arg Gly Val Met Lys Asp Tyr Phe Asp Tyr Trp Gly
225 230 235 240

Gln Gly Thr Leu Val Thr Val Ser Ser
245

<210> 105
<211> 747
<212> DNA
<213> Artificial Sequence

<220>
<223> EGFR ScFv

<400> 105
gccatccagt tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60
atcacttgcc gggcaagtca ggacattagc agtgcttttag tctggtatca gcagaaacca 120
gggaaagctc ctaagctcct gatctatgat gcctccagtt tggaaagtgg ggtcccatca 180
aggttcagcg gcagtgaatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240
gaagattttg caacttatta ctgtcaacag tttaatagtt acccgctcac tttcggcgga 300
gggaccaagg tggagatcaa aggcggaggt ggaagcggag ggggaggatc tggcggcgga 360
ggaagcggag gccaggtgca gctggtggag tctgggggag gcgtggtcca gcctgggagg 420
tccctgagac tctcctgtgc agcgtctgga ttcaccttca gtacctatgg catgcactgg 480
gtccgccagg ctccaggcaa ggggctggag tgggtggcag ttatatggga tgatggaagt 540
tataaatact atggagactc cgtgaagggc cgattcacca tctccagaga caattccaag 600
aacacgctgt atctgcaaat gaacagcctg agagccgagg acacggctgt gtattactgt 660
gcgagagatg gtattactat ggttcgggga gttatgaagg actactttga ctactggggc 720
cagggaaccc tggtcaccgt ctcctca 747

<210> 106
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR ScFv

<400> 106

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

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Tyr
20 25 30

Pro Ile His Trp Val Lys Gln Ala Pro Gly Lys Gly Phe Lys Trp Met
35 40 45

Gly Met Ile Tyr Thr Asp Ile Gly Lys Pro Thr Tyr Ala Glu Glu Phe
50 55 60

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

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

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

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

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

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

Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu His Trp Tyr
165 170 175

Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser
180 185 190

Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
195 200 205

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

Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Trp Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Leu Glu Ile Lys
245

<210> 107
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> EGFR ScFv

<400> 107
cagatccagt tgggtgcagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc 60
tcctgcaagg cctctgggta taccttcaca gaatatccaa tacactgggt gaagcaggct 120
ccaggaaagg gtttcaagt gatgggcatg atatacaccg acattggaaa gccaacatat 180
gctgaagagt tcaagggacg gtttgccttc tctttggaga cctctgccag cactgcctat 240
ttgcagatca acaacctcaa gaatgaggac acggctacat atttctgtgt aagagatcga 300
tatgattccc tctttgacta ctggggccaa ggcaccactc tcacagtctc ctcaggcgga 360
ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgatgt tgtgatgacc 420
caaactccac tctccctgcc tgtcagtctt ggagatcaag cctccatctc ttgcagatct 480
agtcagagcc ttgtacacag taatggaaac acctatttac attggtacct gcagaagcca 540
ggccagtctc caaagctcct gatctacaaa gtttccaacc gattttcttg ggtcccagac 600
aggttcagtg gcagtggatc agggacagat ttcacactca agatcagcag agtggaggct 660
gaggatctgg gagtttattt ctgctctcaa agtacacatg ttccgtggac gttcggtgga 720
ggcaccaagc tggaaatcaa a 741

<210> 108
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR ScFv

<400> 108

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly
130 135 140

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

Tyr Pro Ile His Trp Val Lys Gln Ala Pro Gly Lys Gly Phe Lys Trp
165 170 175

Met Gly Met Ile Tyr Thr Asp Ile Gly Lys Pro Thr Tyr Ala Glu Glu
180 185 190

Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala
195 200 205

Tyr Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe
210 215 220

Cys Val Arg Asp Arg Tyr Asp Ser Leu Phe Asp Tyr Trp Gly Gln Gly
225 230 235 240

Thr Thr Leu Thr Val Ser Ser
245

<210> 109
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> EGFR ScFv

<400> 109
gatgttgatga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
atctcttgca gatctagtca gaggccttgta cacagtaatg gaaacaccta ttacattgg 120
tacctgcaga agccaggcca gtctccaaag ctctgatctt acaaagtttc caaccgattt 180
tctgggggtcc cagacagggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttccg 300
tggacgttcg gtggaggcac caagctggaa atcaaaggcg gaggtggaag cggaggggga 360
ggatctggcg gcggaggaag cggaggccag atccagttgg tgcagtctgg acctgagctg 420
aagaagcctg gagagacagt caagatctcc tgcaaggcct ctgggtatac cttcacagaa 480
tatccaatac actgggtgaa gcaggctcca ggaaagggtt tcaagtggat gggcatgata 540
tacaccgaca ttggaaagcc aacatatgct gaagagttca agggacggtt tgccttctct 600
ttggagacct ctgccagcac tgcctatttg cagatcaaca acctcaagaa tgaggacacg 660
gctacatatt tctgtgtaag agatcgatat gattccctct ttgactactg gggccaaggc 720
accactctca cagtctcctc a 741

<210> 110
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR ScFv

<400> 110

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser His Tyr
20 25 30

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

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

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

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Phe Tyr Cys
85 90 95

Ser Arg Ser Ser Tyr Gly Asn Asn Gly Asp Ala Leu Asp Phe Trp Gly
100 105 110

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Asp Val Val Met Thr Gln
130 135 140

Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
145 150 155 160

Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu
165 170 175

His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr
180 185 190

Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
195 200 205

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

Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Leu Thr Phe
225 230 235 240

Gly Ser Gly Thr Lys Leu Glu Ile Lys
245

<210> 111
<211> 747
<212> DNA
<213> Artificial Sequence

<220>
<223> EGFR ScFv

<400> 111
gaaatgcagc tggtggagtc tgggggaggc ttcgtgaagc ctggagggtc cctgaaactc 60
tcatgtgcag cctctggatt cgctttcagt cactatgaca tgtcttgggt tcgccagact 120
ccgaagcaga ggctggagtg ggtcgcatac attgctagtg gtggtgatat cacctactat 180
gcagacactg tgaagggccg attcaccatc tccagagaca atgcccagaa caccctgtac 240
ctgcaaatga gcagtctgaa gtctgaggac acagccatgt tttactgttc acgatacttc 300
tatggtaaca acggagatgc cctggacttc tgggggtcaag gtacctcagt caccgtcttc 360
tcaggcggag gtggaagcgg agggggagga tctggcggcg gaggaagcgg aggcgatgtt 420
gtgatgaccc aaactccact ctccctgcct gtcagtcttg gagatcaagc ctccatctct 480
tgcagatcta gtcagagcct tgttcacagt aatggaaaca cctatttaca ttggtacctg 540
cagaagccag gccagtctcc aaagctcctg atctacaaag tttccaaccg attttctggg 600
gtcccagaca ggttcagtgg cagtggatca gggacagatt tcacactcaa gatcagcaga 660
gtggaggctg aggatctggg agttttatttc tgctctcaaa gtacacatgt tctcacgttc 720
ggctcgggga caaagttgga aataaaa 747

<210> 112
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR ScFv

<400> 112

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Thr His Val Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser His Tyr
145 150 155 160

Asp Met Ser Trp Val Arg Gln Thr Pro Lys Gln Arg Leu Glu Trp Val
165 170 175

Ala Tyr Ile Ala Ser Gly Gly Asp Ile Thr Tyr Tyr Ala Asp Thr Val
180 185 190

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Gln Asn Thr Leu Tyr
195 200 205

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Phe Tyr Cys
210 215 220

Ser Arg Ser Ser Tyr Gly Asn Asn Gly Asp Ala Leu Asp Phe Trp Gly
 225 230 235 240

Gln Gly Thr Ser Val Thr Val Ser Ser
 245

<210> 113
 <211> 747
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> EGFR ScFv

<400> 113
 gatgttgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
 atctcttgca gatctagtca gagccttggt cacagtaatg gaaacaccta ttacattgg 120
 tacctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt 180
 tctgggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
 agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttctc 300
 acgttcggct cggggacaaa gttggaaata aaaggcggag gtggaagcgg agggggagga 360
 tctggcggcg gaggaagcgg aggcgaaatg cagctggtgg agtctggggg aggcttcgtg 420
 aagcctggag ggtccctgaa actctcatgt gcagcctctg gattcgcttt cagtcactat 480
 gacatgtctt gggttcgcca gactccgaag cagaggctgg agtgggtcgc atacattgct 540
 agtgggtggtg atatcaccta ctatgcagac actgtgaagg gccgattcac catctccaga 600
 gacaatgccc agaacaccct gtacctgcaa atgagcagtc tgaagtctga ggacacagcc 660
 atgttttact gttcacgac ctcctatggt aacaacggag atgccctgga cttctggggt 720
 caaggtacct cagtcaccgt ctcctca 747

<210> 114
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EGFR ScFv

<400> 114

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

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

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

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

Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

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

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

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

Val Ile Leu Ser Val Ser Pro Gly Glu Arg Val Ser Phe Ser Cys Arg
145 150 155 160

Ala Ser Gln Ser Ile Gly Thr Asn Ile His Trp Tyr Gln Gln Arg Thr
165 170 175

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

Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

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

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

Glu Leu Lys

<210> 115
 <211> 729
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> EGFR ScFv

<400> 115
 caggtgcagc tgaagcagtc cggccccggc ctggtgcagc cctcccagtc cctgtccatc 60
 acctgcaccg tgtccggctt ctccctgacc aactacggcg tgcactgggt gcggcagtcc 120
 cccggcaagg gcctggagtg gctgggcgtg atctggtccg gcggcaacac cgactacaac 180
 acccccttca cctcccggct gtccatcaac aaggacaact ccaagtcca ggtgttcttc 240
 aagatgaact ccctgcagtc caacgacacc gccatctact actgcgcccg ggccctgacc 300
 tactacgact acgagttcgc ctactggggc cagggcaccc tggtgaccgt gtccgccggc 360
 ggaggtggaa gcggaggggg aggatctggc ggcgaggaa gcggaggcga catcctgctg 420
 acccagtccc ccgtgaccta gtccgtgtcc cccggcgagc ggggtgtcctt ctcttgccgg 480
 gcctcccagt ccatcggcac caacatccac tggtaccagc agcggaccaa cggctcccc 540
 cggctgctga tcaagtacgc ctccgagtcc atctccggca tcccctccc gttctccggc 600
 tccggctccg gcaccgactt caccctgtcc atcaactccg tggagtccga ggacatcgcc 660
 gactactact gccagcagaa caacaactgg cccaccacct tcggcgccgg caccaagctg 720
 gagctgaag 729

<210> 116
 <211> 244
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> EGFR ScFv

<400> 116

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser His
20 25 30

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

Gly Glu Phe Asn Pro Ser Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Met Thr Val Asp Thr Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Ser Arg Asp Tyr Asp Tyr Asp Gly Arg Tyr 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 Gly Gly Asp Ile Gln Met Thr Gln
130 135 140

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

Cys Ser Ala Ser Ser Ser Val Thr Tyr Met Tyr Trp Tyr Gln Gln Lys
165 170 175

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

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr
195 200 205

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

Cys Gln Gln Trp Ser Ser His Ile Phe Thr Phe Gly Gln Gly Thr Lys
 225 230 235 240

Val Glu Ile Lys

<210> 117
 <211> 731
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> EGFR ScFv

<400> 117
 aggtgcagct ggtgcagtcc ggcgccgagg tgaagaagcc cggcgcctcc gtgaaggtgt 60
 cctgcaaggc ctccggctac accttcacct cccactggat gcactgggtg cggcaggccc 120
 ccggccaggg cctggagtgg atcggcgagt tcaaccctc caacggccgg accaactaca 180
 acgagaagtt caagtccaag gccaccatga ccgtggacac ctccaccaac accgcctaca 240
 tggagctgtc ctccctgcgg tccgaggaca ccgccgtgta ctactgcgcc tcccgggact 300
 acgactacga cggccggtac ttcgactact ggggccaggg caccctggtg accgtgtcct 360
 ccggcggagg tggaagcgga gggggaggat ctggcggcgg aggaagcgga ggcgacatcc 420
 agatgacca gtccccctc tccctgtccg cctccgtggg cgaccgggtg accatcacct 480
 gctccgcctc ctctccgtg acctacatgt actggtacca gcagaagccc ggcaaggccc 540
 ccaagctgct gatctacgac acctccaacc tggcctccgg cgtgccctcc cggttctccg 600
 gctccggctc cggcaccgac tacaccttca ccatctcctc cctgcagccc gaggacatcg 660
 ccacctacta ctgccagcag tggctctccc acatcttcac cttcggccag ggcaccaagg 720
 tggagatcaa g 731

<210> 118
 <211> 243
 <212> PRT
 <213> Artificial Sequence

<220>

<223> EGFR ScFv

<400> 118

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

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

Asp Tyr Tyr Trp Thr Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly His Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr
85 90 95

Cys Val Arg Asp Arg Val Thr Gly Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

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

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

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

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

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

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

Gln His Phe Asp His Leu Pro Leu Ala Phe Gly Gly Gly Thr Lys Val
 225 230 235 240

Glu Ile Lys

<210> 119
 <211> 729
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> EGFR ScFv

<400> 119
 caggtgcagc tgcaggagtc cggccccggc ctggtgaagc cctccgagac cctgtccctg 60
 acctgcaccg tgtccggcgg ctccgtgtcc tccggcgact actactggac ctggatccgg 120
 cagtcccccg gcaagggcct ggagtggatc ggccacatct actactccgg caacaccaac 180
 tacaaccct ccctgaagtc ccggctgacc atctccatcg acacctcaa gaccagttc 240
 tccctgaagc tgcctccgt gaccgccgc gacaccgcca tctactactg cgtgcgggac 300
 cgggtgaccg ggccttcga catctggggc cagggcacca tggtgaccgt gtcctccggc 360
 ggaggtggaa gcggaggggg aggatctggc ggcggaggaa gcggaggcga catccagatg 420
 acccagtccc cctcctccct gtccgcctcc gtgggcgacc gggtgaccat cacctgccag 480
 gcctcccagg acatctcaa ctacctgaac tggtagcagc agaagcccgg caaggcccc 540
 aagctgctga tctacgacgc ctccaacctg gagaccggcg tgccctcccg gttctccggc 600
 tccggctccg gcaccgactt caccttcacc atctcctccc tgcagcccga ggacatcgcc 660
 acctacttct gccagcactt cgaccacctg cccctggcct tcggcggcgg caccaagggtg 720
 gagatcaag 729

<210> 120
 <211> 125
 <212> PRT
 <213> Artificial Sequence

<220>

<223> EGFR VH

<400> 120

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

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

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

Ala Val Ile Trp Asp Asp Gly Ser Tyr Lys Tyr Tyr Gly 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 Asp Gly Ile Thr Met Val Arg Gly Val Met Lys Asp Tyr Phe
100 105 110

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

<210> 121

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR VL

<400> 121

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Phe Asn Ser Tyr Pro Leu
85 90 95

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

<210> 122
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR VH

<400> 122

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

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Tyr
20 25 30

Pro Ile His Trp Val Lys Gln Ala Pro Gly Lys Gly Phe Lys Trp Met
35 40 45

Gly Met Ile Tyr Thr Asp Ile Gly Lys Pro Thr Tyr Ala Glu Glu Phe
50 55 60

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

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

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

Thr Leu Thr Val Ser Ser
115

<210> 123
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR VL

<400> 123

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 124
<211> 121
<212> PRT
<213> Artificial Sequence

<220>

<223> EGFR VH

<400> 124

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser His Tyr
20 25 30

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

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

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

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Phe Tyr Cys
85 90 95

Ser Arg Ser Ser Tyr Gly Asn Asn Gly Asp Ala Leu Asp Phe Trp Gly
100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 125

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR VL

<400> 125

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

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

Thr His Val Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 126
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> EGR VH

<400> 126

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

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Asn Tyr
20 25 30

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

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

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

Lys Met Asn Ser Leu Gln Ser Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

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

Thr Leu Val Thr Val Ser Ala
115

<210> 127
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR VL

<400> 127

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

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Ser Ile Gly Thr Asn
20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Asn Asn Asn Trp Pro Thr
85 90 95

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 128
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR VH

<400> 128

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser His
20 25 30

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

Gly Glu Phe Asn Pro Ser Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Ser Lys Ala Thr Met Thr Val Asp Thr Ser Thr Asn Thr Ala Tyr
65 70 75 80

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

Ala Ser Arg Asp Tyr Asp Tyr Asp Gly Arg Tyr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 129

<211> 106

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR VL

<400> 129

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

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Thr Tyr Met
20 25 30

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

Asp Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

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

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser His Ile Phe Thr
85 90 95

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

<210> 130
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR VH

<400> 130

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

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

Asp Tyr Tyr Trp Thr Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly His Ile Tyr Tyr Ser Gly Asn Thr Asn Tyr Asn Pro Ser
50 55 60

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

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr
85 90 95

Cys Val Arg Asp Arg Val Thr Gly Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser
115

<210> 131
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR VL

<400> 131

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

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

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

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

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

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

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

<210> 132
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-H1

<400> 132

Thr Tyr Gly Met His
1 5

<210> 133
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-H1

<400> 133

Glu Tyr Pro Ile His
1 5

<210> 134
<211> 5
<212> PRT
<213> Artificial SEquence

<220>
<223> EGFR CDR-H1

<400> 134

His Tyr Asp Met Ser
1 5

<210> 135
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-H1

<400> 135

Asn Tyr Gly Val His
1 5

<210> 136
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-H1

<400> 136

Ser His Trp Met His
1 5

<210> 137

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR CDR-H1

<400> 137

Ser Gly Asp Tyr Tyr Trp Thr
1 5

<210> 138

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR CDR-H2

<400> 138

Val Ile Trp Asp Asp Gly Ser Tyr Lys Tyr Tyr Gly Asp Ser Val Lys
1 5 10 15

Gly

<210> 139

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR CDR-H2

<400> 139

Met Ile Tyr Thr Asp Ile Gly Lys Pro Thr Tyr Ala Glu Glu Phe Lys
1 5 10 15

Gly

<210> 140
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-H2

<400> 140

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

Gly

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

<220>
<223> EGFR CDR-H2

<400> 141

Val	Ile	Trp	Ser	Gly	Gly	Asn	Thr	Asp	Tyr	Asn	Thr	Pro	Phe	Thr	Ser
1				5					10					15	

<210> 142
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-H2

<400> 142

Glu	Phe	Asn	Pro	Ser	Asn	Gly	Arg	Thr	Asn	Tyr	Asn	Glu	Lys	Phe	Lys
1				5					10					15	

Ser

<210> 143
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-H2

<400> 143

His	Ile	Tyr	Tyr	Ser	Gly	Asn	Thr	Asn	Tyr	Asn	Pro	Ser	Leu	Lys	Ser
1				5					10					15	

<210> 144
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-H3

<400> 144

Asp	Gly	Ile	Thr	Met	Val	Arg	Gly	Val	Met	Lys	Asp	Tyr	Phe	Asp	Tyr
1				5					10					15	

<210> 145
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-H3

<400> 145

Asp	Arg	Tyr	Asp	Ser	Leu	Phe	Asp	Tyr
1				5				

<210> 146
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-H3

<400> 146

Ser	Ser	Tyr	Gly	Asn	Asn	Gly	Asp	Ala	Leu	Asp	Phe
1				5					10		

<210> 147
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-H3

<400> 147

Ala Leu Thr Tyr Tyr Asp Tyr Glu Phe Ala Tyr
1 5 10

<210> 148
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-H3

<400> 148

Arg Asp Tyr Asp Tyr Asp Gly Arg Tyr Phe Asp Tyr
1 5 10

<210> 149
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-H3

<400> 149

Asp Arg Val Thr Gly Ala Phe Asp Ile
1 5

<210> 150
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-L1

<400> 150

Arg Ala Ser Gln Asp Ile Ser Ser Ala Leu Val
1 5 10

<210> 151
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-L1

<400> 151

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

<210> 152
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-L1

<400> 152

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

<210> 153
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-L1

<400> 153

Arg	Ala	Ser	Gln	Ser	Ile	Gly	Thr	Asn	Ile	His
1				5				10		

<210> 154
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-L1

<400> 154

Ser Ala Ser Ser Ser Val Thr Tyr Met Tyr
1 5 10

<210> 155
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-L1

<400> 155

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 156
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-L2

<400> 156

Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 157
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-L2

<400> 157

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 158
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR CDR-L2

<400> 158

Tyr Ala Ser Glu Ser Ile Ser
1 5

<210> 159

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR CDR-L2

<400> 159

Asp Thr Ser Asn Leu Ala Ser
1 5

<210> 160

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR CDR-L2

<400> 160

Asp Ala Ser Asn Leu Glu Thr
1 5

<210> 161

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR CDR-L3

<400> 161

Gln Gln Phe Asn Ser Tyr Pro Leu Thr
1 5

<210> 162

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR CDR-L3

<400> 162

Ser Gln Ser Thr His Val Pro Trp Thr
1 5

<210> 163

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR CDR-L3

<400> 163

Ser Gln Ser Thr His Val Leu Thr
1 5

<210> 164

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR CDR-L3

<400> 164

Gln Gln Asn Asn Asn Trp Pro Thr Thr
1 5

<210> 165

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR CDR-L3

<400> 165

Gln Gln Trp Ser Ser His Ile Phe Thr
1 5

<210> 166

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> EGFR CDR-L3

<400> 166

Gln His Phe Asp His Leu Pro Leu Ala
1 5

<210> 167

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<223> pan-HLA ScFv

<400> 167

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

Ser Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

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

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

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

Lys Met Asn Ser Leu Gln Ala Asp Asp Thr Ala Ile Tyr Tyr Cys Ala
85 90 95

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

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Ser Ile Val Met Thr Gln Thr
130 135 140

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

Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Gln Ser Pro Ile Cys Leu Leu Ile Tyr Tyr Ala Ser Asn Arg
180 185 190

Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Tyr Gly Thr Asp
195 200 205

Phe Thr Phe Thr Ile Ser Thr Val Gln Ala Glu Asp Leu Ala Val Tyr
210 215 220

Phe Cys Gln Gln Asp Tyr Ser Ser Pro Pro Trp Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Leu Glu Ile Arg
245

<210> 168
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> pan-HLA ScFv

<400> 168
caggtgcagc tgaagcagtc aggacctggc ctagtgcagc cctcacagag cctgtccctg 60
acctgcacag tctctggttt ctcatctaact agttatggcg tacactgggt tcgccagcct 120
ccaggaaagg gtctggagtg gctgggagtg atctggagtg gtggaagcac agactataat 180
gctgctttca tatccagact gagcatcagg aaggacaact ccaagagcca agtcttcttt 240
aaaatgaaca gtctgcaagc tgatgacaca gccatatact actgtgccag aacctttact 300
acgtctacct cggcctgggt tgcttactgg ggccaaggga ctctgggtcac tgtctctgca 360
ggcgggagtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cagcatcgtg 420
atgacccaga ctccaaaatt cctgcttgtg tctgcgggag acagagtcac catcacttgc 480

aaggcgagtc agtctgtgag caacgacgta gcttggtatc agcagaaacc agggcaatct 540
cctatctgtc tcctgatcta ctatgcatct aatcggtata caggggtccc tgataggttc 600
accggaagtg gatatgggac agatttcact ttcacatca gcaccgtgca ggctgaagat 660
cttgcagtat atttctgtca acaggattat agtagtcctc cgtggacttt cggcggaggg 720
accaagttgg agatcaga 738

<210> 169
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> pan-HLA ScFv

<400> 169

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

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

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

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

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

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

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

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

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

Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr
180 185 190

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

Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr
210 215 220

Cys Gln Gln Asp Tyr Ser Ser Pro Pro Trp Thr Phe Gly Gly Gly Thr
225 230 235 240

Lys Val Glu Ile Lys
245

<210> 170
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> pan-HLA ScFv

<400> 170
caggtgcagc tgcaggagtc cggacctggc ctagtgaagc cctcacagac cctgtccctg 60
acctgcacag tctctggttt ctcattaact agctatggtg tacactggat tagacagcct 120
ccaggaaagg gtctggagtg gattggagtg atctggagtg gtggaagcac agactataat 180
gctgctttca tatccagagt gaccatcagc gtggacacct ccaagaacca attctccctt 240
aaactgagca gtgtgacagc tgccgacaca gccgtatact actgtgccag aacctttact 300
acgtctacct cggcctggtt tgcttactgg ggccaaggga ctctggtcac tgtctcttca 360
ggcggaggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgacatcgtg 420

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

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

Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr
180 185 190

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

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

Cys Gln Gln Asp Tyr Ser Ser Pro Pro Trp Thr Phe Gly Gly Gly Thr
225 230 235 240

Lys Val Glu Ile Lys
245

<210> 172
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> pan-HLA ScFv

<400> 172
gagggtgcagc tgctggagtc cggaggtggc ctagtgcagc ccggagggag cctgctgcctg 60
agctgctgcag cctctgggttt ctcattaact agctatggtg tacactgggt tagacaggct 120
ccaggaaagg gtctggagtg ggtagcgtg atctggagtg gtggaagcac agactataat 180
gctgctttca tatccagatt taccatcagc cgggacaact ccaagaacac actctacctt 240
caaatgaaca gtttgagagc tgaagacaca gccgtatact actgtgccag aacctttact 300
acgtctacct cggcctgggt tgcttactgg ggccaaggga ctctgggtcac tgtctcttca 360

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

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

Pro Leu Ser Leu Ser Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys
145 150 155 160

Lys Ala Ser Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Leu Gln Lys
165 170 175

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr
180 185 190

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

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

Cys Gln Gln Asp Tyr Ser Ser Pro Pro Trp Thr Phe Gly Gly Gly Thr
225 230 235 240

Lys Val Glu Ile Lys
245

<210> 174
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> pan-HLA ScFv

<400> 174
caggtgcagc tgcaggagtc cggacctggc ctagtgaagc cctcagaaac cctgtccctg 60
acctgcacag tctctggttt ctcattaact agctatggtg tacactggat tagacagcct 120
ccaggaaagg gtctggagtg gattggagtg atctggagtg gtggaagcac agactataat 180
gctgctttca tatccagagt gaccatcagc aggacacct ccaagaacca attctccctt 240
aaactgagca gtgtgacagc tgccgacaca gccgtatact actgtgccag aacctttact 300

acgtctacct cggcctgggtt tgcttactgg ggccaaggga ctctggtcac tgtctcttca 360
 ggcggagggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgacatcgtg 420
 atgaccaga ctccactttc cctgtctgtg actccgggac agccagccag catcagttgc 480
 aaggcgagtc agtctgtgag caacgacgta gcttggtatc tgcagaaacc agggcaatct 540
 cctcaactcc tgatctacta tgcataat cggtatacag gggtccctga taggttcagc 600
 ggaagtggat ctgggacaga tttcactttg aagatcagca gggtggaggc tgaagatgtt 660
 ggagtatatt actgtcaaca ggattatagt agtcctccgt ggactttcgg cggagggacc 720
 aaggtggaga tcaaa 735

<210> 175
 <211> 245
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> pan-HLA ScFv

<400> 175

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

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

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

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

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

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

Lys Thr Phe Thr Thr Ser Thr Ser Ala Trp Phe Ala Tyr Trp Gly Gln
 100 105 110

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Glu Ile Val Leu Thr Gln Ser
130 135 140

Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145 150 155 160

Arg Ala Ser Gln Ser Val Ser Asn Asp Leu Ala Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr
180 185 190

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

Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr
210 215 220

Cys Gln Gln Asp Tyr Ser Ser Pro Pro Trp Thr Phe Gly Gln Gly Thr
225 230 235 240

Lys Val Glu Ile Lys
245

<210> 176
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> pan-HLA ScFv

<400> 176
caggtgcagc tgggtggagtc cggaggtggc gtagtgcagc ccggaaggag cctg'gcctg 60
agctgcgcag tctctggttt ctcatctaat agctatggta tgcactgggt tagacaggct 120
ccaggaaagg gtctggagtg ggttgcagtg atctggagtg gtggaagcac agactataat 180
gctgctttca tatccagatt taccatcagc cgggacaact ccaagaacac actctacctt 240

caaatgaaca gtttgagagc tgaagacaca gccgtatact actgtgccaa aacctttact 300
 acgtctacct cggcctgggtt tgcttactgg ggccaaggga ctctggtcac tgtctcttca 360
 ggcggagggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgagatcgtg 420
 ctgaccaga gtccagctac cctgtctctg tctccgggag agagagccac cctcagttgc 480
 agggcgagtc agtctgtgag caacgaccta gcttggtatc agcagaaacc agggcaagct 540
 cctagactcc tgatctacta tgcattctaat cggtatacag gggtcctga taggttcagc 600
 ggaagtggat ctgggacaga tttcactctc accatcagca gcctggagcc tgaagatttt 660
 gcagtatatt actgtcaaca ggattatagt agtcctccgt ggactttcgg ccaagggacc 720
 aagtgaggaga tcaaa 735

<210> 177
 <211> 245
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> pan-HLA ScFv

<400> 177

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

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

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

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

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

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

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

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

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

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

Gln Ala Ser Gln Ser Val Ser Asn Asp Leu Asn Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Asn Arg Tyr
180 185 190

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

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

Cys Gln Gln Asp Tyr Ser Ser Pro Pro Trp Thr Phe Gly Gly Gly Thr
225 230 235 240

Lys Val Glu Ile Lys
245

<210> 178
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> pan-HLA ScFv

<400> 178
caggtgcagc tgggtggagtc cggaggtggc gtagtgcagc ccggaaggag cctgcgcctg 60
agctgcgcag tctctggttt ctcattaact agctatggta tgcactgggt tagacaggct 120
ccaggaaagg gtctggagtg ggttgcagtg atctggagtg gtggaagcac agactataat 180

gctgctttca tatccagatt taccatcagc cgggacaact ccaagaacac actctacctt	240
caaatgaaca gtttgagagc tgaagacaca gccgtatact actgtgccag aacctttact	300
acgtctacct cggcctgggtt tgcttactgg ggccaaggga ctctgggtcac tgtctcttca	360
ggcggaggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgacatccag	420
atgaccaga gtccaagctc cctgtctgcg tctgtgggag acagagtcac catcacttgc	480
caggcgagtc agtctgtgag caacgaccta aattgggtatc agcagaaacc agggaaagct	540
cctaaactcc tgatctacta tgcattctaat cggtatacag gggtccctga taggttcagc	600
ggaagtggat ctgggacaga tttcactttc accatcagca gcctgcagcc tgaagatatt	660
gcaacatatt actgtcaaca ggattatagt agtcctccgt ggactttcgg cggaggggacc	720
aaggtggaga tcaaa	735

<210> 179
 <211> 741
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HLA-A*02 antigen binding domain

<400> 179	
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc	60
atctcttgca gatctagtca gagcattgta catagtaatg gaaacaccta tttagaatgg	120
tacctgcaga aaccaggcca gtctccaaag ctctgatctt acaaagtttc caaccgattt	180
tctgggggtcc cagacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc	240
agtagagtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acatgttcct	300
cggacgtccg gtggaggcac caagctggaa atcaaaggcg gaggtggaag cggaggggga	360
ggatctggcg gcggaggaag cggaggccag gtccagctgc agcagtctgg acctgagctg	420
gtgaagcctg gggcttcagt gaggatatcc tgcaaggctt ctggctacac cttcacaagt	480
taccatatac attgggtgaa gcagaggcct ggacagggac ttgagtggat tggatggatt	540
tatcctggaa atgttaatac tgagtacaat gagaagttca agggcaaggc cacactgact	600
gcagacaaat cgtccagcac agcctacatg cacctcagca gcctgacctc tgaggactct	660
gcggtctatt tctgtgccag agaggagatt acctatgcta tggactactg ggggtcaagga	720

acctcagtca ccgtgtcctc a 741

<210> 180
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A*02 antigen binding domain

<400> 180
caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc agtgaaggtt 60
tcctgcaagg cttctggata caccttcact agctatcata tacattgggt gcgccaggcc 120
cccggacaag ggcttgagtg gatgggatgg atctaccctg gcaatgttaa cacagaatat 180
aatgagaagt tcaagggcaa agccaccatt accgcggaca aatccacgag cacagcctac 240
atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagggaggaa 300
attacctacg ctatggacta ctggggccag ggaaccacag tcaccgtgtc ctcaggcgga 360
ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgagat tgtattgacc 420
cagagcccag gcaccctgag cctctctcca ggagagcggg ccaccctcag ttgtagatcc 480
agtcagagta ttgtacacag taatgggaac acctatttgg aatggtatca gcagaaacca 540
ggtcaagccc caagattgct catctacaaa gtctctaaca gatttagtgg tattccagac 600
aggttcagcg gttccggaag tgggtactgat ttcaccctca cgatctccag gctcgagcca 660
gaagatttcg ccgtttatta ctgttttcaa ggttcacatg tgccgcgcac attcggtggg 720
ggtactaaag tagaaatcaa a 741

<210> 181
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A*02 antigen binding domain

<400> 181
caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc agtgaaggtt 60
tcctgcaagg cttctggata caccttcact agctatcata tacattgggt gcgccaggcc 120
cccggacaag ggcttgagtg gatgggatgg atctaccctg gcaatgttaa cacagaatat 180

aatgagaagt tcaagggcaa agccaccatt accgcggaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagggaggaa	300
attacctacg ctatggacta ctggggccag ggaaccacag tcaccgtgtc ctcaggcgga	360
ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgacat tgtaatgacc	420
cagacccac tcagcctgcc cgtcactcca ggagagccgg ccagcatcag ttgtagatcc	480
agtcagagta ttgtacacag taatgggaac acctatttgg aatggtatct gcagaaacca	540
ggtcaatccc cacaattgct catctacaaa gtctctaaca gatttagtgg tgtaccagac	600
aggttcagcg gttccggaag tgggtactgat ttcaccctca agatctccag ggtcgaggca	660
gaagatgtcg gcgtttatta ctgttttcaa ggttcacatg tgccgcgcac attcggtggg	720
ggtactaaag tagaaatcaa a	741

<210> 182
 <211> 741
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HLA-A*02 antigen binding domain

<400> 182	
gaggtgcagc tggtggagtc tgggggtggg ctggtgaagc ctgggggctc actgaggctt	60
tcctgcgcgg cttctggata caccttcact agctatcata tacattgggt gcgccaggcc	120
cccggaaaag ggcttgagtg ggtgggatgg atctaccctg gcaatgttaa cacagaatat	180
aatgagaagt tcaagggcag attcaccatt agcagggacg attccaagaa cacactctac	240
ctgcagatga acagcctgaa aactgaagac acggctgtgt attactgtgc gagggaggaa	300
attacctacg ctatggacta ctggggccag ggaaccacag tcaccgtgtc ctcaggcgga	360
ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgacat tcaaatgacc	420
cagagcccat ccagcctgag cgcactctgta ggtgaccggg tcaccatcac ttgtagatcc	480
agtcagagta ttgtacacag taatgggaac acctatttgg aatggtatca gcagaaacca	540
ggtaaagccc caaaattgct catctacaaa gtctctaaca gatttagtgg tgtaccaagc	600
aggttcagcg gttccggaag tgggtactgat ttcaccctca cgatctcctc tctccagcca	660
gaagatttcg ccacttatta ctgttttcaa ggttcacatg tgccgcgcac attcggtggg	720

ggtactaaag tagaaatcaa a 741

<210> 183
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A*02 antigen binding domain

<400> 183
caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc agtgaaggtt 60
tcctgcaagg cttctggata caccttcact agctatcata tacattgggt gcgccaggcc 120
cccggacaag ggcttgagtg gatcggatgg atctaccctg gcaatgttaa cacagaatat 180
aatgagaagt tcaagggcaa agccaccatt accgcggacg aatccacgaa cacagcctac 240
atggagctga gcagcctgag atctgaagac acggctgtgt attactgtgc gagggaggaa 300
attacctacg ctatggacta ctggggccag ggaaccctgg tcaccgtgtc ctcaggcgga 360
ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgacat tcaaattgacc 420
cagagcccat ccaccctgag cgcattctgta ggtgaccggg tcaccatcac ttgtagatcc 480
agtcagagta ttgtacacag taatgggaac acctatttgg aatggatatca gcagaaacca 540
ggtaaagccc caaaattgct catctacaaa gtctctaaca gatttagtgg tgtaccagcc 600
aggttcagcg gttccggaag tgggtactgaa ttcaccctca cgatctcctc tctccagcca 660
gatgatttcg ccacttatta ctgttttcaa ggttcacatg tgccgcgcac attcggtcag 720
ggtactaaag tagaagtcaa a 741

<210> 184
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A*02 antigen binding domain

<400> 184
caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctgggtcctc agtgaaggtt 60
tcctgcaagg cttctggata caccttcact agctatcata tgcattgggt gcgccaggcc 120
cccggacaag ggcttgagtg gatcggatac atctaccctg gcaatgttaa cacagaatat 180

aatgagaagt tcaagggcaa agccaccctt accgcggaca aatccacgaa cacagcctac	240
atggagctga gcagcctgag atctgaagac acggctgtgt atttctgtgc gagggaggaa	300
attacctacg ctatggacta ctggggccag ggaaccctgg tcaccgtgtc ctcaggcgga	360
ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgacgt tcaaatgacc	420
cagagcccat ccaccctgag cgcattctgta ggtgaccggg tcaccatcac ttgtagctcc	480
agtcagagta ttgtacacag taatgggaac acctatatgg aatggtatca gcagaaacca	540
ggtaaagccc caaaattgct catctacaaa gtctctaaca gatttagtgg tgtaccagac	600
aggttcagcg gttccggaag tgggtactgaa ttcaccctca cgatctcttc tctccagcca	660
gatgatttcg ccacttatta ctgtcatcaa ggttcacatg tgccgcgcac attcggtcag	720
ggtactaaag tagaagtcaa a	741

<210> 185
 <211> 741
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HLA-A*02 antigen binding domain

<400> 185	
caggtgcagc tgcagcagtc tgggcctgag ctggtgaagc ctggggcctc agtgaagatg	60
tcctgcaagg cttctggata caccttcact agctatcata tccagtgggt gaagcagagg	120
cctggacaag ggcttgagtg gatcggatgg atctaccctg gcgatggtag tacacagtat	180
aatgagaagt tcaagggcaa aaccaccctt accgcggaca aatcctccag cacagcctac	240
atgttgctga gcagcctgac ctctgaagac tctgctatct atttctgtgc gagggagggg	300
acctactacg ctatggacta ctggggccag ggaacctcag tcaccgtgtc ctcaggcgga	360
ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgatgt tttgatgacc	420
cagactccac tctccctgcc tgtctctctt ggagaccaag tctccatctc ttgtagatcc	480
agtcagagta ttgtacacag taatgggaac acctatttag aatggtatct gcagaaacca	540
ggtcagtctc caaagttgct catctacaaa gtctctaaca gatttagtgg tgtaccagac	600
aggttcagcg gttccggaag tgggtactgat ttcaccctca agatctcgag agtggaggct	660
gaggatctgg gaggtttatta ctgttttcaa ggttcacatg tgccgcgcac attcgggtgga	720

ggtactaaac tggaaatcaa a 741

<210> 186
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A*02 antigen binding domain

<400> 186
cagctgcagc tgcaggagtc tggggccggg ctggtgaagc cttcggaac gctgagcctc 60
acctgcacgg tttctggata caccttcacc agctatcata tccagtggat ccgacagccc 120
cctggaaaag ggcttgagtg gatcggatgg atctaccctg gcgatggttc aacacagtac 180
aatgagaagt tcaagggcag agccacgatt agcgtggaca catccaagaa ccaattctcc 240
ctgaacctgg acagcgtgag tgctgcggac acggccattt attactgtgc gagagaggga 300
acttactacg ctatggacta ctggggcaaa gggagcacgg tcaccgtgtc ctcaggcgga 360
ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgacat ccagatgacc 420
cagagcccaa gctccctgag tgcgtccgtg ggcgaccgag tgaccatcac ttgcagatcc 480
tctcagtcca tcgtgcactc caacggcaac acgtacctcg agtggtacca gcagaagccc 540
gggaaggccc cgaaactgct catctacaag gtgagcaacc ggttctccgg cgtccccagc 600
cgcttctcag ggtccggctc ggggacggat ttcaccttca cgattagcag cttgcagccc 660
gaagacatcg ccacgtacta ctgctttcag ggaagtcacg tgccgcgtac cttcgggccg 720
ggcacgaaag tggatattaa g 741

<210> 187
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A*02 antigen binding domain

<400> 187
gaggtgcagc tggtgcagtc tggggccgag ctgaagaagc ctgggtcctc ggtgaagggtg 60
tcctgcaagg cttctggata caccttcacc agctatcata tccagtgggt aaaacaggcc 120
cctggacaag ggcttgagtg gatcggatgg atctaccctg gcgatggttc aacacagtac 180

aatgagaagt tcaagggcaa agccacgctt accgtggaca aatccacgaa cacagcctac	240
atggagctga gcagcctgag atctgaggac acggccgtat attactgtgc gagagaggga	300
acttactacg ctatggacta ctggggccaa gggaccctgg tcaccgtgtc ctcaggcgga	360
ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgacat ccagatgacc	420
cagagcccat ccaccctgag tgcgtccgtg ggcgaccgcg tgaccatcac ttgcagatcc	480
tctcagtcca tcgtgcactc caacggcaac acgtacctcg agtggtacca gcagaagccc	540
gggaaggccc cgaaactgct catctacaag gtgagcaacc ggttctccgg cgtccccagc	600
cgcttctcag ggtccggctc ggggacggat ttcaccctca cgattagcag cttgcagccc	660
gatgacttcg ccacgtacta ctgctttcag ggaagtcacg tgccgcgtac cttcgggcag	720
ggcacgaaag tggaagttaa g	741

<210> 188
 <211> 741
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> HLA-A*02 antigen binding domain

<400> 188	
caggtgcagc tggtgcagtc tggggccgag gtgaagaagc ctgggtcctc ggtgaagggtg	60
tcctgcaagg cttctggata caccttcacc agctatcata tccagtgggt acgacaggcc	120
cctggacaag ggcttgagtg gatgggatgg atctaccctg gcgatggttc aacacagtac	180
aatgagaagt tcaagggcag agtcacgatt accgcggaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac acggccgtat attactgtgc gagagaggga	300
acttactacg ctatggacta ctggggccaa gggaccacgg tcaccgtgtc ctcaggcgga	360
ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgagat cgtcctgacc	420
cagagcccag ggaccctgag tttgtccccg ggcgagcgcg cgaccctcag ttgcagatcc	480
tctcagtcca tcgtgcactc caacggcaac acgtacctcg agtggtacca gcagaagccc	540
gggcaggccc cgcgactgct catctacaag gtgagcaacc ggttctccgg catccccgac	600
cgcttctcag ggtccggctc ggggacggat ttcaccctca cgattagccg cttggagccc	660
gaagacttcg ccgtgtacta ctgctttcag ggaagtcacg tgccgcgtac cttcgggggg	720

ggcacgaaag tggaaattaa g 741

<210> 189
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A*02 antigen binding domain

<400> 189
caggtgaccc tgaagcagtc tggggccgag gtgaagaagc ctgggtcctc ggtgaaggtg 60
tcctgcacgg cttctggata caccttcacc agctatcatg tcagctgggt acgacaggcc 120
cctggacaag ggcttgagtg gttgggaagg atctaccctg gcgatggttc aacacagtac 180
aatgagaagt tcaagggcaa agtcacgatt accgcggaca aatccatgga cacatccttc 240
atggagctga ccagcctgac atctgaggac acggccgtat attactgtgc gagagaggga 300
acttactacg ctatggacct ctggggccaa gggaccctgg tcaccgtgtc ctcaggcgga 360
ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgagat cgtcctgacc 420
cagagcccag ggaccctgag tttgtccccg ggcgagcgcg cgaccctcag ttgcagatcc 480
tctcagtcca tcgtgcactc caacggcaac acgtacctcg cgtggtacca gcagaagccc 540
gggcaggccc cgcgactgct catctccaag gtgagcaacc ggttctccgg cgtccccgac 600
cgcttctcag ggtccggctc ggggacggat ttcaccctca cgattagccg cttggagccc 660
gaagacttcg ccgtgtacta ctgccaacag ggaagtcacg tgccgcgtac cttcgggggg 720
ggcacgaaag tggaaattaa g 741

<210> 190
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> HLA-A*02 antigen binding domain

<400> 190
caggtgcagc tgggtgcagtc tggggccgag gtgaagaagc ctggggcctc ggtgaaggtg 60
tcctgcaagg cttctggata caccttcacc agctatcata tgcaactgggt acgacaggcc 120
cctggacaaa ggcttgagtg gatgggatgg atctaccctg gcgatggttc aacacagtac 180

aatgagaagt tcaagggcaa agtcacgatt acccgggaca catccgcgag cacagcctac	240
atggagctga gcagcctgag atctgaggac acggccgtat attactgtgc gagagaggga	300
acttactacg ctatggacta ctggggccaa gggaccctgg tcaccgtgtc ctcaggcgga	360
ggtggaagcg gagggggagg atctggcggc ggaggaagcg gaggcgacat cgtcatgacc	420
cagacccac tgtccctgcc tgtgaccccg ggcgagcccg cgagcatcag ttgcagatcc	480
tctcagtcca tcgtgcactc caacggcaac acgtacctcg actggtacct gcagaagccc	540
gggcagtccc cgcaactgct catctacaag gtgagcaacc ggttctccgg cgtccccgac	600
cgcttctcag ggtccggctc ggggacggat ttcaccctca agattagccg cgtggaggcc	660
gaagacgtcg gcgtgtacta ctgcatgcag ggaagtcacg tgccgcgtac cttcgggggg	720
ggcacgaaag tggaaattaa g	741

<210> 191
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HA-1 variant H peptide

<400> 191

Val	Leu	His	Asp	Asp	Leu	Leu	Glu	Ala
1					5			

<210> 192
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P2A self cleaving peptide

<400> 192

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

Pro Gly Pro

<210> 193
<211> 608
<212> PRT
<213> Artificial Sequence

<220>
<223> HA-1H TCR alpha and beta

<400> 193

Met Val Lys Ile Arg Gln Phe Leu Leu Ala Ile Leu Trp Leu Gln Leu
1 5 10 15

Ser Cys Val Ser Ala Ala Lys Asn Glu Val Glu Gln Ser Pro Gln Asn
20 25 30

Leu Thr Ala Gln Glu Gly Glu Phe Ile Thr Ile Asn Cys Ser Tyr Ser
35 40 45

Val Gly Ile Ser Ala Leu His Trp Leu Gln Gln His Pro Gly Gly Gly
50 55 60

Ile Val Ser Leu Phe Met Leu Ser Ser Gly Lys Lys Lys His Gly Arg
65 70 75 80

Leu Ile Ala Thr Ile Asn Ile Gln Glu Lys His Ser Ser Leu His Ile
85 90 95

Thr Ala Ser His Pro Arg Asp Ser Ala Val Tyr Ile Cys Ala Val Arg
100 105 110

Ser Val Ser Gly Ala Gly Ser Tyr Gln Leu Thr Phe Gly Lys Gly Thr
115 120 125

Lys Leu Ser Val Ile Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr
130 135 140

Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val
165 170 175

Tyr Ile Thr Asp Lys Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys
180 185 190

Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala
195 200 205

Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser
210 215 220

Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr
225 230 235 240

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

Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu
260 265 270

Trp Ser Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala
275 280 285

Gly Asp Val Glu Glu Asn Pro Gly Pro Met Gly Thr Ser Leu Leu Cys
290 295 300

Trp Met Ala Leu Cys Leu Leu Gly Ala Asp His Ala Asp Thr Gly Val
305 310 315 320

Ser Gln Asn Pro Arg His Lys Ile Thr Lys Arg Gly Gln Asn Val Thr
325 330 335

Phe Arg Cys Asp Pro Ile Ser Glu His Asn Arg Leu Tyr Trp Tyr Arg
340 345 350

Gln Thr Leu Gly Gln Gly Pro Glu Phe Leu Thr Tyr Phe Gln Asn Glu
355 360 365

Ala Gln Leu Glu Lys Ser Arg Leu Leu Ser Asp Arg Phe Ser Ala Glu
370 375 380

Arg Pro Lys Gly Ser Phe Ser Thr Leu Glu Ile Gln Arg Thr Glu Gln
385 390 395 400

Gly Asp Ser Ala Met Tyr Leu Cys Ala Ser Ser Ile Asp Ser Phe Asn
405 410 415

Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr Val Leu Glu Asp Leu
420 425 430

Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala
435 440 445

Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly
450 455 460

Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu
465 470 475 480

Val His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro
485 490 495

Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser
500 505 510

Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln
515 520 525

Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys
530 535 540

Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys
545 550 555 560

Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile
565 570 575

Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val
580 585 590

Ser Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser Arg Gly
595 600 605

<210> 194
<211> 1827
<212> DNA
<213> Artificial Sequence

<220>
<223> HA-1(H) TCR alpha and beta

<400> 194
atggtgaaga tccggcaatt tttgttggct attttgtggc ttcagctaag ctgtgtaagt 60
gccgcaaaa atgaagtgga gcagagtcct cagaacctga ctgcccagga aggagaatth 120
atcacaatca actgcagtta ctcggttagga ataagtcct tacactggct gcaacagcat 180
ccaggaggag gcattgtttc cttgtttatg ctgagctcag ggaagaagaa gcatggaaga 240
ttaattgccca caataaacat acaggaaaag cacagctccc tgcacatcac agcctcccat 300
cccagagact ctgccgtcta catctgtgct gtcagaagcg tgtccggggc cggctcctac 360
cagctcacct ttgggaaggg gaccaaatta tcagtcattc caaatatcca gaaccctgac 420
cctgccgtgt accagctgag agactctaaa tccagtgaca agtctgtctg cctattcacc 480
gattttgatt ctcaaacaaa tgtgtcacia agtaaggatt ctgatgtgta tatcacagac 540
aaatgtgtgc tagacatgag gtctatggac ttcaagagca acagtgtgtg ggcctggagc 600
aacaatctg actttgcatg tgcaaacgcc ttcaacaaca gcattattcc agaagacacc 660
ttcttcccca gccagaaaag ttcctgtgat gtcaagctgg tcgagaaaag ctttgaaaca 720
gatacgaacc taaactttca aaacctgtca gtgattgggt tccgaatcct cctcctgaaa 780
gtggccgggt ttaatctgct catgacgctg cggctgtggt ccagcggatc cggagccacc 840
aacttcagcc tgctgaagca ggccggcgac gtggaggaga accccggccc catgggcacc 900
agcctcctct gctggatggc cctgtgtctc ctgggggcag atcacgcaga tactggagtc 960
tcccagaacc ccagacacia gatcaciaag aggggacaga atgtaacttt caggtgtgat 1020
ccaatttctg aacacaaccg cttttattgg taccgacaga ccctggggca gggcccagag 1080
tttctgactt acttcagaa tgaagctcaa ctagaaaaat caaggctgct cagtgatcgg 1140
ttctctgcag agaggcctaa gggatctttc tccaccttgg agatccagcg cacagagcag 1200
ggggactcgg ccatgtatct ctgtgccagc agcatcgact ctttcaacga gcagttcttc 1260
gggccgggca ccaggctcac ggtcctcgag gacctgaaaa acgtgtttcc acccgaggtc 1320
gctgtgtttg agccatcaga agcagagatc tcccacaccc aaaaggccac actggtgtgc 1380

ctggccacag gcttctaccc cgaccacgtg gagctgagct ggtgggtgaa tgggaaggag 1440
 gtgcacagtg gggctctgcac agacccgcag cccctcaagg agcagcccgc cctcaatgac 1500
 tccagatact gcctgagcag ccgcctgagg gtgtcggcca ccttctggca gaacccccgc 1560
 aaccacttcc gctgtcaagt ccagttctac gggctctcgg agaatgacga gtggaccag 1620
 gatagggcca aacctgtcac ccagatcgtc agcgccgagg cctggggtag agcagactgt 1680
 ggcttcacct ccgagtctta ccagcaaggg gtcctgtctg ccaccatcct ctatgagatc 1740
 ttgctaggga aggccacctt gtatgccgtg ctggtcagtg ccctcgtgct gatggccatg 1800
 gtcaagagaa aggattccag aggctag 1827

<210> 195
 <211> 440
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Ftc alpha LIR1 HA-1H

<400> 195

Met Val Lys Ile Arg Gln Phe Leu Leu Ala Ile Leu Trp Leu Gln Leu
 1 5 10 15

Ser Cys Val Ser Ala Ala Lys Asn Glu Val Glu Gln Ser Pro Gln Asn
 20 25 30

Leu Thr Ala Gln Glu Gly Glu Phe Ile Thr Ile Asn Cys Ser Tyr Ser
 35 40 45

Val Gly Ile Ser Ala Leu His Trp Leu Gln Gln His Pro Gly Gly Gly
 50 55 60

Ile Val Ser Leu Phe Met Leu Ser Ser Gly Lys Lys Lys His Gly Arg
 65 70 75 80

Leu Ile Ala Thr Ile Asn Ile Gln Glu Lys His Ser Ser Leu His Ile
 85 90 95

Thr Ala Ser His Pro Arg Asp Ser Ala Val Tyr Ile Cys Ala Val Arg
 100 105 110

Ser Val Ser Gly Ala Gly Ser Tyr Gln Leu Thr Phe Gly Lys Gly Thr
115 120 125

Lys Leu Ser Val Ile Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr
130 135 140

Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val
165 170 175

Tyr Ile Thr Asp Lys Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys
180 185 190

Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala
195 200 205

Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser
210 215 220

Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr
225 230 235 240

Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Val Ile Gly Ile Leu
245 250 255

Val Ala Val Ile Leu Leu Leu Leu Leu Leu Leu Phe Leu Ile
260 265 270

Leu Arg His Arg Arg Gln Gly Lys His Trp Thr Ser Thr Gln Arg Lys
275 280 285

Ala Asp Phe Gln His Pro Ala Gly Ala Val Gly Pro Glu Pro Thr Asp
290 295 300

Arg Gly Leu Gln Trp Arg Ser Ser Pro Ala Ala Asp Ala Gln Glu Glu
305 310 315 320

Asn Leu Tyr Ala Ala Val Lys His Thr Gln Pro Glu Asp Gly Val Glu
325 330 335

Met Asp Thr Arg Ser Pro His Asp Glu Asp Pro Gln Ala Val Thr Tyr
340 345 350

Ala Glu Val Lys His Ser Arg Pro Arg Arg Glu Met Ala Ser Pro Pro
355 360 365

Ser Pro Leu Ser Gly Glu Phe Leu Asp Thr Lys Asp Arg Gln Ala Glu
370 375 380

Glu Asp Arg Gln Met Asp Thr Glu Ala Ala Ala Ser Glu Ala Pro Gln
385 390 395 400

Asp Val Thr Tyr Ala Gln Leu His Ser Leu Thr Leu Arg Arg Glu Ala
405 410 415

Thr Glu Pro Pro Pro Ser Gln Glu Gly Pro Ser Pro Ala Val Pro Ser
420 425 430

Ile Tyr Ala Thr Leu Ala Ile His
435 440

<210> 196
<211> 1279
<212> DNA
<213> Artificial Sequence

<220>
<223> Ftc r alpha LIR1 HA-1H

<400> 196
atggtgaaga tccggcaatt tttgttggct attttgtggc ttcagctaag ctgtgtaagt 60
gccgcaaaa atgaagtgga gcagagtcct cagaacctga ctgccagga aggagaattt 120
atcacaatca actgcagtta ctcggttagga ataagtcct tacactggct gcaacagcat 180
ccaggaggag gcattgtttc cttgtttatg ctgagctcag ggaagaagaa gcatggaaga 240
ttaattgcc aataaacat acaggaaaag cacagctccc tgcacatcac agcctcccat 300
cccagagact ctgccgtcta catctgtgct gtcagaagcg tgtccggggc cggctcctac 360
cagctcacct ttgggaaggg gaccaaatta tcagtcattc caaatatcca gaaccctgac 420

cctgccgtgt accagctgag agactctaaa tccagtgaca agtctgtctg cctattcacc	480
gatttttgatt ctcaaacaaa tgtgtcacia agtaaggatt ctgatgtgta tatcacagac	540
aaatgtgtgc tagacatgag gtctatggac ttcaagagca acagtgtctgt ggcctggagc	600
aacaaatctg actttgcatg tgcaaacgcc ttcaacaaca gcattattcc agaagacacc	660
ttcttcccca gccagaaaag ttcctgtgat gtcaagctgg tcgagaaaag ctttgaaaca	720
gatacgaacc taaactttca aaacctgtca gttgtgatcg gcatcttggt ggccgtcatc	780
ctactgctcc tcctcctcct cctcctcttc ctcatcctcc gacatcgacg tcagggcaaa	840
cactggacat cgacccagag aaaggctgat ttccaacatc ctgcaggggc tgtggggcca	900
gagcccacag acagaggcct gcagtggagg tccagcccag ctgccgatgc ccaggaagaa	960
aacctctatg ctgccgtgaa gcacacacag cctgaggatg ggggtggagat ggacactcgg	1020
agcccacacg atgaagaccc ccaggcagtg acgtatgccg aggtgaaaca ctccagacct	1080
aggagagaaa tggcctctcc tccttcccca ctgtctgggg aattcctgga cacaaaggac	1140
agacaggcgg aagaggacag gcagatggac actgaggctg ctgcatctga agccccccag	1200
gatgtgacct acgcccagct gcacagcttg accctcagac gggaggcaac tgagcctcct	1260
ccatcccagg aagggccct	1279

<210> 197
 <211> 466
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fcrr beta LIR1 HA-1H

<400> 197

Met	Gly	Thr	Ser	Leu	Leu	Cys	Trp	Met	Ala	Leu	Cys	Leu	Leu	Gly	Ala
1				5				10						15	

Asp	His	Ala	Asp	Thr	Gly	Val	Ser	Gln	Asn	Pro	Arg	His	Lys	Ile	Thr
			20					25					30		

Lys	Arg	Gly	Gln	Asn	Val	Thr	Phe	Arg	Cys	Asp	Pro	Ile	Ser	Glu	His
		35					40					45			

Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60

Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80

Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
85 90 95

Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
100 105 110

Ser Ser Ile Asp Ser Phe Asn Glu Gln Phe Phe Gly Pro Gly Thr Arg
115 120 125

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

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln
260 265 270

Gly Val Leu Ser Val Val Ile Gly Ile Leu Val Ala Val Ile Leu Leu
275 280 285

Leu Leu Leu Leu Leu Leu Leu Phe Leu Ile Leu Arg His Arg Arg Gln
290 295 300

Gly Lys His Trp Thr Ser Thr Gln Arg Lys Ala Asp Phe Gln His Pro
305 310 315 320

Ala Gly Ala Val Gly Pro Glu Pro Thr Asp Arg Gly Leu Gln Trp Arg
325 330 335

Ser Ser Pro Ala Ala Asp Ala Gln Glu Glu Asn Leu Tyr Ala Ala Val
340 345 350

Lys His Thr Gln Pro Glu Asp Gly Val Glu Met Asp Thr Arg Ser Pro
355 360 365

His Asp Glu Asp Pro Gln Ala Val Thr Tyr Ala Glu Val Lys His Ser
370 375 380

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

Phe Leu Asp Thr Lys Asp Arg Gln Ala Glu Glu Asp Arg Gln Met Asp
405 410 415

Thr Glu Ala Ala Ala Ser Glu Ala Pro Gln Asp Val Thr Tyr Ala Gln
420 425 430

Leu His Ser Leu Thr Leu Arg Arg Glu Ala Thr Glu Pro Pro Pro Ser
435 440 445

Gln Glu Gly Pro Ser Pro Ala Val Pro Ser Ile Tyr Ala Thr Leu Ala
450 455 460

Ile His
465

<210> 198
<211> 1401
<212> DNA
<213> Artificial Sequence

<220>
<223> Fcγr beta LIR1 HA-1H

<400> 198
atgggcacca gcctcctctg ctggatggcc ctgtgtctcc tgggggcaga tcacgcagat 60
actggagtct cccagaacct cagacacaag atcacaaaga ggggacagaa tgtaactttc 120
agggtgtgat caatttctga acacaaccgc ctttattggg accgacagac cctggggcag 180
ggcccagagt ttctgactta cttccagaat gaagctcaac tagaaaaatc aaggctgctc 240
agtgatcggg tctctgcaga gaggcctaag ggatctttct ccaccttgga gatccagcgc 300
acagagcagg gggactcggc catgtatctc tgtgccagca gcatcgactc cttcaacgag 360
cagttcttcg ggccgggcac caggctcacg gtcctcgagg acctgaaaaa cgtgttccca 420
cccgaggctg ctgtgtttga gccatcagaa gcagagatct cccacacca aaaggccaca 480
ctggtgtgcc tggccacagg cttctacccc gaccacgtgg agctgagctg gtgggtgaat 540
gggaaggagg tgcacagtgg ggtctgcaca gaccgcagc ccctcaagga gcagcccgcc 600
ctcaatgact ccagatactg cctgagcagc cgcctgaggg tgtcggccac cttctggcag 660
aacccccgca accacttccg ctgtcaagtc cagttctacg ggctctcgga gaatgacgag 720
tggaccagg atagggccaa acctgtcacc cagatcgtca gcgccaggc ctggggtaga 780
gcagactgtg gcttcacctc cgagtcttac cagcaagggg tcctgtctgt tgtgatcggc 840
atcttggtgg ccgtcatcct actgctcctc ctctctctcc tcctcttctt catcctccga 900
catcgacgtc agggcaaaca ctggacatcg acccagagaa aggctgattt ccaacatcct 960
gcaggggctg tggggccaga gccacagac agaggcctgc agtgagggtc cagcccagct 1020
gccgatgcc aggaagaaaa cctctatgct gccgtgaagc acacacagcc tgaggatggg 1080
gtggagatgg acactcggag cccacacgat gaagaccccc aggcagtgac gtatgccgag 1140
gtgaaacact ccagacctag gagagaaatg gcctctcctc cttccccact gtctggggaa 1200
ttcctggaca caaaggacag acaggcggaa gaggacaggc agatggacac tgaggctgct 1260
gcatctgaag ccccccagga tgtgacctac gccagctgc acagcttgac cctcagacgg 1320
gaggcaactg agcctcctcc atcccaggaa gggccctctc cagctgtgcc cagcatctac 1380

gccactctgg ccatccacta g

1401

<210> 199
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> HA-1H TCR alpha

<400> 199

Met Val Lys Ile Arg Gln Phe Leu Leu Ala Ile Leu Trp Leu Gln Leu
1 5 10 15

Ser Cys Val Ser Ala Ala Lys Asn Glu Val Glu Gln Ser Pro Gln Asn
20 25 30

Leu Thr Ala Gln Glu Gly Glu Phe Ile Thr Ile Asn Cys Ser Tyr Ser
35 40 45

Val Gly Ile Ser Ala Leu His Trp Leu Gln Gln His Pro Gly Gly Gly
50 55 60

Ile Val Ser Leu Phe Met Leu Ser Ser Gly Lys Lys Lys His Gly Arg
65 70 75 80

Leu Ile Ala Thr Ile Asn Ile Gln Glu Lys His Ser Ser Leu His Ile
85 90 95

Thr Ala Ser His Pro Arg Asp Ser Ala Val Tyr Ile Cys Ala Val Arg
100 105 110

Ser Val Ser Gly Ala Gly Ser Tyr Gln Leu Thr Phe Gly Lys Gly Thr
115 120 125

Lys Leu Ser Val Ile Pro Asn Ile Gln Asn Pro Asp Pro Ala Val Tyr
130 135 140

Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr
145 150 155 160

Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val
165 170 175

Tyr Ile Thr Asp Lys Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys
180 185 190

Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala
195 200 205

Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser
210 215 220

Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr
225 230 235 240

Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser
245 250

<210> 200
<211> 276
<212> PRT
<213> Artificial Sequence

<220>
<223> HA-1H TCR beta

<400> 200

Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Thr Gly Val Ser Gln Asn Pro Arg His Lys Ile Thr
20 25 30

Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
35 40 45

Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60

Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80

Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
85 90 95

Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
100 105 110

Ser Ser Ile Asp Ser Phe Asn Glu Gln Phe Phe Gly Pro Gly Thr Arg
115 120 125

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

Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr
145 150 155 160

Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser
165 170 175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro
180 185 190

Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu
195 200 205

Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn
210 215 220

His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu
225 230 235 240

Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu
245 250 255

Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln
260 265 270

Gly Val Leu Ser
275

<210> 201

<211> 750

<212> DNA
<213> Artificial Sequence

<220>
<223> HA-1H TCR alpha

<400> 201
atggtgaaga tccggcaatt tttgttggct attttgtggc ttcagctaag ctgtgtaagt 60
gccgcaaaa atgaagtgga gcagagtcct cagaacctga ctgcccagga aggagaattt 120
atcacaatca actgcagtta ctcggtagga ataagtgcct tacactggct gcaacagcat 180
ccaggaggag gcattgtttc cttgtttatg ctgagctcag ggaagaagaa gcatggaaga 240
ttaattgcca caataaacat acaggaaaag cacagctccc tgcacatcac agcctcccat 300
cccagagact ctgccgtcta catctgtgct gtcagaagcg tgtccggggc cggctcctac 360
cagctcacct ttgggaaggg gaccaaatta tcagtcattc caaatatcca gaaccctgac 420
cctgccgtgt accagctgag agactctaaa tccagtgaca agtctgtctg cctattcacc 480
gattttgatt ctcaaacaaa tgtgtcacia agtaaggatt ctgatgtgta tatcacagac 540
aaatgtgtgc tagacatgag gtctatggac ttcaagagca acagtgtgtg ggcctggagc 600
aacaatctg actttgcatg tgcaaacgcc ttcaacaaca gcattattcc agaagacacc 660
ttcttcccca gccagaaaag ttcctgtgat gtcaagctgg tcgagaaaag ctttgaaaca 720
gatacgaacc taaactttca aaacctgtca 750

<210> 202
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<223> HA-1H TCR beta

<400> 202
atgggcacca gcctcctctg ctggatggcc ctgtgtctcc tgggggcaga tcacgcagat 60
actggagtct cccagaacct cagacacaag atcacaaaga ggggacagaa tgtaactttc 120
aggtgtgatc caatttctga acacaaccgc ctttattggg accgacagac cctggggcag 180
ggcccagagt ttctgactta cttccagaat gaagctcaac tagaaaaatc aaggctgctc 240
agtgatcggg tctctgcaga gaggcctaag ggatctttct ccaccttgga gatccagcgc 300
acagagcagg gggactcggc catgtatctc tgtgccagca gcatcgactc cttcaacgag 360

cagttcttcg ggccgggcac caggctcacg gtcctcgagg acctgaaaaa cgtgttccca	420
cccgagggtcg ctgtgtttga gccatcagaa gcagagatct cccacacca aaaggccaca	480
ctggtgtgcc tggccacagg cttctacccc gaccacgtgg agctgagctg gtgggtgaat	540
gggaaggagg tgcacagtgg ggtctgcaca gacccgcagc ccctcaagga gcagcccgcc	600
ctcaatgact ccagatactg cctgagcagc cgcctgaggg tgcggccac cttctggcag	660
aacccccgca accacttccg ctgtcaagtc cagttctacg ggctctcgga gaatgacgag	720
tggaccagg atagggcaa acctgtcacc cagatcgtca gcgccgaggc ctggggtaga	780
gcagactgtg gcttcacctc cgagtcttac cagcaagggg tcctgtct	828

<210> 203
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> NY-ESO CDR

<400> 203

Cys	Ala	Ser	Ser	Leu	Gly	Leu	Gly	Tyr	Glu	Gln	Tyr	Phe
1				5					10			

<210> 204
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> NY-ESO CDR

<400> 204

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

Asp	Glu	Gln	Phe
			20

<210> 205
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>

<223> NY-ESO CDR

<400> 205

Cys Ala Ser Ser Leu Arg Arg Asp Asn Glu Gln Phe
1 5 10

<210> 206

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A3 CDR

<400> 206

Cys Ala Ser Ser Leu Glu Val Leu Leu Gly Ala Asp Phe Pro Asp Thr
1 5 10 15

Gln Tyr Phe

<210> 207

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A3 CDR

<400> 207

Cys Ala Ser Ser Phe Pro Ala Gly His Gly Ala Asp Leu Asp Asn Glu
1 5 10 15

Gln Phe

<210> 208

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A3 CDR

<400> 208

Cys Ala Ser Ser Glu Ile Thr Gly Arg Ile Gly Glu Gln Phe
1 5 10

<210> 209

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A3 CDR

<400> 209

Cys Ala Ser Ser Leu Gly Gly Asp Glu Leu Gly Ala Asp Gly Asn Glu
1 5 10 15

Gln Phe

<210> 210

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<223> NY-ESO-1 ScFv

<400> 210

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

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

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

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

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

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser
100 105 110

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

Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu
130 135 140

Ser Cys Ala Ala Ser Gly Phe Thr Val Tyr Asp Tyr Met Ser Trp Val
145 150 155 160

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

Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
180 185 190

Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu
195 200 205

Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Ser Tyr Tyr
210 215 220

Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser
225 230 235 240

Ser

<210> 211
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<223> NY-ESO-1 ScFv

<400> 211
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc

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

Ala Arg Ile Pro Phe Gly Asp Trp Trp Tyr Phe Asp Leu Trp Gly Arg
100 105 110

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

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

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

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
180 185 190

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

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

Cys Gln Gln Ser Tyr Ser Phe Val Leu Thr Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Glu Ile Lys

<210> 213
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> MAGE-A3 antigen binding domain

<400> 213
caggtgcagc tgcaggaaag cggccctggc ctggtgaaac ccagcgacac cctgagcctg 60
acctgcgccg tgtccggcta cagcatcagc agcagcaatt ggtggggctg gatcagacag 120
ccccctggca agggcctgga atggatcggc tacatctact acagcggcag cacctactac 180
aaccacagcc tgaagtccag agtgaccatg agcgtggaca ccagcaagaa ccagttcagc 240
ctgaagctga gcagcgtgac cgccgtcgat accgctgtgt attactgtgc gagaataccc 300
tttggggatt ggtggtactt cgatctctgg ggccgtggca ccctggtcac tgtgtcctca 360
ggcggagggtg gaagcggagg gggaggatct ggccggcgag gaagcggagg cgacatccag 420
atgaccacaga gccccagcag cctgagcgcc agcgtgggag acagagtgc catcacctgt 480
cgggccagcc agtcgatcag cagctacctg aactggtatc agcagaagcc cggcaaggcc 540
cccaagctgc tgatctacgc cgccagctcc ctgcagagcg gcgtgccaaag cagattcagc 600
ggcagcggct ccggcaccga cttcacctg accatcagca gcctgcagcc cgaggacttc 660
gccacctact actgccagca gagttacagt ttcgttctca ctttcggcgg agggaccaag 720
gtggagatca aa 732

<210> 214
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A3 antigen binding domain

<400> 214

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

Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu Leu
20 25 30

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

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

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

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

Ala Thr Asp Leu Tyr Ser Ser Ser Trp Tyr Cys Asp Ala Phe Asp Ile
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

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

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
180 185 190

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

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

Thr Tyr Tyr Cys Gln Gln Ser Trp Ala Ser Thr Pro Leu Thr Phe Gly
225 230 235 240

Gly Gly Thr Lys Val Glu Ile Lys
245

<210> 215

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<223> MAGE-A3 antigen binding domain

<400> 215

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caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ctggcgccctc cgtgaagggtg      60
tcctgcaagg tgtccggcta caccctgacc gagctgtcga tgcactgggt ccgccaggca      120
cctggcaagg gactggaatg gatgggcggc tttgaccccg aggacggcga gacaatctac      180
gcccagaaat tccagggcag agtgaccatg accgaggaca ccagcaccga caccgcctac      240
atggaactga gcagcctgcg gagcgaggac accgctgtgt attactgtgc aacagatctg      300
tatagcagca gctggtactg tgatgctttt gatatctggg gccaaaggac aatggtcacc      360
gtgtcctcag gcggagggtg aagcggaggg ggaggatctg gcggcggagg aagcggaggc      420
gacatccaga tgaccagag ccccgagcagc ctgagcgcca gcgtgggcga cagagtgacc      480
atcacctgtc gggccagcca gtcgatcagc agctacctga actggtatca gcagaagccc      540
ggcaaggccc ccaagctgct gatctacgcc gccagctccc tgcaagcgcg cgtgccaagc      600
agattcagcg gcagcggctc cggcaccgac ttcaccctga ccatcagcag cctgcagccc      660
gaggacttcg ccacctacta ctgccagcag agttggggcca gcacccctct cactttcggc      720
ggagggacca aggtggagat caaa      744
```

<210> 216

<211> 245

<212> PRT

<213> Artificial Sequence

<220>

<223> HPV E6 antigen binding domain

<400> 216

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala 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 Glu Asn Gly Val Val Lys Trp Tyr Phe Asp Leu Trp Gly Arg
100 105 110

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

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

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

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
180 185 190

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

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

Cys Gln Gln Ser Tyr Ser Thr Pro Leu Phe Pro Phe Gly Gly Gly Thr
225 230 235 240

Lys Val Glu Ile Lys
245

<210> 217
<211> 735
<212> DNA
<213> Artificial Sequence

<220>

<223> HPV E6 antigen binding domain

<400> 217

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gaagtgcagc tggtggaaag cggcggaggc ctggtgcagc ctggcggcag cctgagactg      60
tcttgcgccg ccagcggctt caccttcagc agctactgga tgcactgggt ccgccaggcc      120
cctggcaagg gactggtctg ggtgtctcga atcaacagcg acggcagcag caccagctac      180
gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa caccctgtac      240
ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc cagggagaac      300
ggcgtggtga agtggtactt cgacctgtgg ggccgtggca ccctggtcac tgtgtcctca      360
ggcggagggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgacatccag      420
atgaccaga gccccagcag cctgagcgcc agcgtgggag acagagtga catcacctgt      480
cgggccagcc agtcgatcag cagctacctg aactggatat agcagaagcc cggcaaggcc      540
cccaagctgc tgatctacgc cgccagctcc ctgcagagcg gcgtgccaag cagattcagc      600
ggcagcggct ccggcaccga cttcacctg accatcagca gcctgcagcc cgaggacttc      660
gccacctact actgccagca gagttacagt acccctctct ttcccttcgg cggagggacc      720
aaggtggaga tcaaa                                         735
```

<210> 218

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<223> HPV E6 antigen binding domain

<400> 218

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

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

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

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

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

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

Ala Lys Asp Gly Arg Gly Ser Pro Phe Tyr Gly Gly Ala Phe Asp Ile
100 105 110

Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

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

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
180 185 190

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

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

Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 219

<211> 741

<212> DNA
<213> Artificial Sequence

<220>
<223> HPV E6 antigen binding domain

<400> 219
gaagtgcagc tggtggaaag cggcggaggc ctggtgcagc ccggtcgaag cctgagactg 60
agctgcgccg ccagcggctt cacctttgac gactacgcca tgcactgggt ccgccaggcc 120
cctggcaagg gactggaatg ggtgtccggc atcagctgga acagcggcag catcggctac 180
gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240
ctgcagatga acagcctgcg ggccgaggac accgccttgt attactgtgc caaggacggc 300
aggggctccc ctttctacgg cggcgccttc gacatctggg gccaaggagc aatggtcacc 360
gtgtcctcag gcggagggtgg aagcggaggg ggaggatctg gcggcggagg aagcggaggc 420
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 480
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 540
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 600
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 660
gaagattttg caacttacta ctgtcaacag agttacagta cccctctcac tttcggcggc 720
ggaacaaagg tggagatcaa g 741

<210> 220
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> HPV E7 antigen binding domain

<400> 220

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

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

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

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

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

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

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

Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
145 150 155 160

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
165 170 175

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
180 185 190

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
195 200 205

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
210 215 220

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

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
245 250

<210> 221
<211> 753
<212> DNA
<213> Artificial Sequence

<220>
<223> HPV E7 antigen binding domain

<400> 221
gaagtgcagc tgggtggaaag cggcggaggc ctggtgaaac ctggcggcag cctgagactg 60
agctgcgccg ccagcggcctt caccttctcg aacgcctgga tgagctgggt ccgccaggcc 120
cctggcaagg gactggaatg ggtcggacgg atcaagagca agaccgacgg cggcaccacc 180
gactacgctg cccccgtgaa gggccggttc accatcagcc gggacgacag caagaacacc 240
ctgtacctgc agatgaacag cctgaaaacc gaggacaccg ccgtgtatta ctgtaccacc 300
tcctacgatt accttctcaa tccttatcgt tggaaactggt tcgaccctg gggccaggga 360
accctggtca ccgtgtcctc aggcggagggt ggaagcggag ggggaggatc tggcggcgga 420
ggaagcggcg gagacatcca gatgaccag tctccatcct ccctgtctgc atctgtagga 480
gacagagtca ccatcacttg ccgggcaagt cagagcatta gcagctatct aaattggtat 540
cagcagaaac cagggaaagc ccctaagctc ctgatctatg ctgcatccag tttgcaaagt 600
ggggtcccat caaggttcag tggcagtgga tctgggacag atttcactct caccatcagc 660
agtctgcaac ctgaagattt tgcaacttac tactgtcaac agagttacag taccctcttc 720
actttcggcg gcggaacaaa ggtggagatc aag 753

<210> 222
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A3 antigen binding domain

<400> 222

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Asp Met Asp Thr Phe Ser Met Val Thr Leu Phe Asp Tyr Trp
100 105 110

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

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

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

Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln
165 170 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
180 185 190

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

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

Tyr Tyr Cys Gln Gln Ser Tyr Ser Trp Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 223
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> MAGE-A3 antigen binding domain

<400> 223
caggtgcagc tgggtgcagtc tggcgccgaa gtgaagaaac ccggcagcag cgtgaagggtg 60
tcctgcaagg ccagcggcgg caccttcagc agctacgcca tcagctgggt ccgccaggct 120
cctggacagg gactggaatg gatgggcggc atcatcccca tcttcggcac cgccaactac 180
gcccagaaat tccagggcag agtgaccatc accgccgacg agagcaccag caccgcctac 240
atggaactga gcagccttcg aagcgaggac accgctgtgt attactgtgc cagggacatg 300
gacaccttct ccatgggtgac cctgttcgac tactggggcc agggcaccct ggtcaccgtg 360
tcctcaggcg gaggtggaag cggaggggga ggatctggcg gcggaggaag cggaggcgac 420
atccagatga cccagagccc cagcagcctg agcgccagcg tgggcgacag agtgaccatc 480
acctgtcggg ccagccagtc gatcagcagc tacctgaact ggtatcagca gaagcccggc 540
aaggcccca agctgctgat ctacgccgcc agctccctgc agagcggcgt gccaaagcaga 600
ttcagcggca gcggctccgg caccgacttc accctgacca tcagcagcct gcagcccag 660
gacttcgcca cctactactg ccagcagagt tacagttggc ctctcacttt cggcggaggg 720
accaaggtgg agatcaaa 738

<210> 224
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> KRAS G12V antigen binding domain

<400> 224

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
50 55 60

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ser Tyr Asp Glu Leu Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

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

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

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

Arg Ala Ser Gln Ser Ile Trp Thr Ser Tyr Leu Asn Trp Tyr Gln Gln
165 170 175

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

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

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

Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225 230 235 240

Lys Val Glu Ile Lys
245

<210> 225
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> KRAS G12V antigen binding domain

<400> 225
caggtcacac tgagagagtc cggccctgcc ctggtgaaac ccaccagac cctgaccctg 60
acatgcacct tcagcggctt cagcctgagc accagcggga tgtgcgtgtc ctggattcga 120
cagccccctg gcaaggccct ggaatggctg gccctgattg actgggacga cgacaagtac 180
tacagcacca gcctgaaaac ccggctgacc atcagcaagg acaccagcaa gaaccaggtg 240
gtgctgacca tgaccaacat ggaccccgctg gacaccgcca cgtattactg tgcacggagt 300
tacgacgagc tctactactt tgactactgg ggccaggga ccctgggtcac cgtgtcctca 360
ggcggagggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgacatccag 420
atgaccaga gccccagctc cctctctgca tctgtgggcg acagagtac catcacctgt 480
cgggccagcc agtcgatctg gaccagctac ctgaactggt atcagcagaa gcccggaag 540
gcccccaagc tgctgatcta cgccgccagc tccctgcaga gcggcgtgcc aagcagattc 600
agcggcagcg gctccggcac cgacttcacc ctgaccatca gcagcctgca gcccgaggac 660
ttcgccacct actactgcca gcagagttac agtaccctc tcactttcgg cggagggacc 720
aaggtggaga tcaaa 735

<210> 226
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 226

Gly Gly Gly Gly Ser
1 5

<210> 227
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 227

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 228
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 228

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 229
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 229

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 230
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 230

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 231
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> linker

<400> 231

Gly Gly Gly Ser
1

<210> 232
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> KRAS ScFv

<400> 232

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

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

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

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

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

Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

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

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
145 150 155 160

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr
165 170 175

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
180 185 190

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

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

Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly
225 230 235 240

Gly Thr Lys Val Glu Ile Lys
245

<210> 233
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> KRAS ScFv

<400> 233
caggtgcagc tgggtggaaag cggcggaggc ctggtgaaac ctggcggcag cctgagactg 60
agctgcgccg ccagcggctt caccttcagc gactactaca tgagctggat cagacaggcc 120
cctggcaagg gactggaatg ggtgtcctac atcagcagca gcggctcgac catctactac 180

gccgacagcg tgaagggccg gttcaccatc agccgggaca acgccaagaa cagcctgtac 240
 ctgcagatga acagcctgcg ggccgaggac accgccgtgt attactgtgc cagggacttc 300
 accagggact actactacta ctactacatg gacgtgtggg gcaaaggac cacggtcacc 360
 gtgtcctcag gcggaggtgg aagcggaggg ggaggatctg gcggcggagg aagcggagggc 420
 gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 480
 atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 540
 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 600
 aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 660
 gaagattttg caacttacta ctgtcaacag agttacagta cccctctcac tttcggcggc 720
 ggaacaaagg tggagatcaa g 741

<210> 234
 <211> 244
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRAS ScFv

<400> 234

Gln	Val	Thr	Leu	Arg	Glu	Ser	Gly	Pro	Ala	Leu	Val	Lys	Pro	Thr	Gln
1				5					10					15	
Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	Ser	Gly	Phe	Ser	Leu	Ser	Thr	Ser
			20					25					30		
Gly	Met	Cys	Val	Ser	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Ala	Leu	Glu
		35					40					45			
Trp	Leu	Ala	Leu	Ile	Asp	Trp	Asp	Asp	Asp	Lys	Tyr	Tyr	Ser	Thr	Ser
	50					55					60				
Leu	Lys	Thr	Arg	Leu	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Asn	Gln	Val
65					70					75				80	
Val	Leu	Thr	Met	Thr	Asn	Met	Asp	Pro	Val	Asp	Thr	Ala	Thr	Tyr	Tyr
				85					90					95	

Cys Ala Arg Ser Tyr Asp Glu Leu Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

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

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

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

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
180 185 190

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

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

Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Glu Ile Lys

<210> 235
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> KRAS ScFv

<400> 235
caggtcacac tgaagagatc cggccctgcc ctggtgaaac ccaccagac cctgaccctg 60
acatgcacct tcagcggctt cagcctgagc accagcggga tgtgcgtgtc ctggattcga 120

cagccccctg gcaaggccct ggaatggctg gccctgattg actgggacga cgacaagtac	180
tacagcacca gcctgaaaac ccggctgacc atcagcaagg acaccagcaa gaaccaggtg	240
gtgctgacca tgaccaacat ggaccccgtg gacaccgcca cgtattactg tgcacggagt	300
tacgacgagc tctactactt tgactactgg ggccaggga ccctgggtcac cgtgtcctca	360
ggcggaggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgacatccag	420
atgacccagt ctccatcctc cctgtctgca tctgtaggag acagagtcac catcacttgc	480
cgggcaagtc agagcattag cagctattta aattggtatc agcagaaacc agggaaagcc	540
cctaagctcc tgatctatgc tgcattccagt ttgcaaagtg ggggtcccatc aaggttcagt	600
ggcagtggtg ctgggacaga tttcactctc accatcagca gtctgcaacc tgaagatttt	660
gcaacttact actgtcaaca gagttacagt acccctctca ctttcggcgg cggaacaaag	720
gtggagatca ag	732

<210> 236
 <211> 245
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRAS ScFv

<400> 236

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

Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	Ser	Gly	Phe	Ser	Leu	Ser	Thr	Ser
			20					25					30		

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

Trp	Leu	Ala	Leu	Ile	Asp	Trp	Asp	Asp	Asp	Lys	Tyr	Tyr	Ser	Thr	Ser
	50					55					60				

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ser Tyr Asp Glu Leu Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

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

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

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

Arg Ala Ser Gln Ser Ile Trp Thr Ser Tyr Leu Asn Trp Tyr Gln Gln
165 170 175

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

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

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

Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225 230 235 240

Lys Val Glu Ile Lys
245

<210> 237
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> KRAS ScFv

<400> 237
caggtcacac tgagagagtc cggccctgcc ctggtgaaac ccaccagac cctgaccctg

acatgcacct tcagcggctt cagcctgagc accagcggga tgtgcgtgtc ctggattcga	120
cagccccctg gcaaggccct ggaatggctg gccctgattg actgggacga cgacaagtac	180
tacagcacca gcctgaaaac ccggctgacc atcagcaagg acaccagcaa gaaccaggtg	240
gtgctgacca tgaccaacat ggaccccgctg gacaccgcca cgtattactg tgcacggagt	300
tacgacgagc tctactactt tgactactgg ggccagggaa ccctggtcac cgtgtcctca	360
ggcggaggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgacatccag	420
atgaccaga gccccagctc cctctctgca tctgtgggcg acagagtga catcacctgt	480
cgggccagcc agtcgatctg gaccagctac ctgaactggt atcagcagaa gcccggaag	540
gcccccaagc tgctgatcta cgccgccagc tccctgcaga gcggcgtgcc aagcagattc	600
agcggcagcg gctccggcac cgacttcacc ctgaccatca gcagcctgca gcccgaggac	660
ttgccacct actactgcca gcagagttac agtaccctc tcactttcgg cggagggacc	720
aaggtggaga tcaaa	735

<210> 238
 <211> 244
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRAS ScFv

<400> 238

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

Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	Ser	Gly	Phe	Ser	Leu	Ser	Thr	Ser
			20					25					30		

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

Trp	Leu	Ala	Leu	Ile	Asp	Trp	Asp	Asp	Asp	Lys	Tyr	Tyr	Ser	Thr	Ser
	50					55					60				

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

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ser Tyr Asp Glu Leu Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

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

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

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

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
180 185 190

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

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

Cys Gln Gln Ser Tyr Ser Thr Arg Leu Thr Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Glu Ile Lys

<210> 239
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> KRAS ScFv

<400> 239
caggtcacac tgagagagtc cggccctgcc ctggtgaaac ccaccagac cctgaccctg 60
acatgcacct tcagcggcctt cagcctgagc accagcggga tgtgcgtgtc ctggattcga 120
cagccccctg gcaaggccctt ggaatggctg gccctgattg actgggacga cgacaagtac 180
tacagcacca gcctgaaaac ccggctgacc atcagcaagg acaccagcaa gaaccaggtg 240
gtgctgacca tgaccaacat ggaccccgctg gacaccgcca cgtattactg tgcacggagt 300
tacgacgagc tctactactt tgactactgg ggccagggaa ccctggtcac cgtgtcctca 360
ggcggagggtg gaagcggagg gggaggatct ggcggcggag gaagcggagg cgacatccag 420
atgaccaga gccccagctc cctctctgca tctgtgggag acagagtac catcacctgt 480
cgggccagcc agtcgatcag cagctacctg aactgggtatc agcagaagcc cggcaaggcc 540
cccaagctgc tgatctacgc cgccagctcc ctgcagagcg gcgtgccaag cagattcagc 600
ggcagcggct ccggcaccga cttcaccctg accatcagca gcctgcagcc cgaggacttc 660
gccacctact actgccagca gagttacagt acccggtca ctttcggcgg agggaccaag 720
gtggagatca aa 732

<210> 240
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> KRAS TCR alpha

<400> 240

Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val Gln Ile
1 5 10 15

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

Leu His Glu Gly Thr Asp Ser Ala Leu Arg Cys Asn Phe Thr Thr Thr
35 40 45

Met Arg Ser Val Gln Trp Phe Arg Gln Asn Ser Arg Gly Ser Leu Ile
50 55 60

Ser Leu Phe Tyr Leu Ala Ser Gly Thr Lys Glu Asn Gly Arg Leu Lys
65 70 75 80

Ser Ala Phe Asp Ser Lys Glu Arg Arg Tyr Ser Thr Leu His Ile Arg
85 90 95

Asp Ala Gln Leu Glu Asp Ser Gly Thr Tyr Phe Cys Ala Ala Asp Ser
100 105 110

Ser Asn Thr Gly Tyr Gln Asn Phe Tyr Phe Gly Lys Gly Thr Ser Leu
115 120 125

Thr Val Ile Pro Asn Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu
130 135 140

Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe
145 150 155 160

Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile
165 170 175

Thr Asp Lys Cys Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn
180 185 190

Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile
195 200 205

Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp
210 215 220

Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe
225 230 235 240

Gln Asn Leu Ser

<210> 241

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> KRAS TCR alpha

<400> 241

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atgcagagga acctgggagc tgtgctgggg attctgtggg tgcagatttg ctgggtgaga      60
ggggatcagg tggagcagag tccttcagcc ctgagcctcc acgagggaac cgattctgct      120
ctgagatgca attttacgac caccatgagg agtgtgcagt ggttccgaca gaattccagg      180
ggcagcctca tcagtttggt ctacttggct tcaggaacaa aggagaatgg gaggctaaag      240
tcagcatttg attctaagga gcggcgctac agcacctgc acatcaggga tgcccagctg      300
gaggactcag gcacttactt ctgtgctgct gactcttcga acacgggtta ccagaacttc      360
tatTTTggga aaggaacaag tttgactgtc attcCaaca tccagaaccc agaacctgct      420
gtgtaccagt taaaagatcc tcggtctcag gacagcacc cctgcctggt caccgacttt      480
gactcccaaa tcaatgtgcc gaaaaccatg gaatctggaa cgttcacac tgacaaatgt      540
gtgctggaca tgaaagctat ggattccaag agcaatgggg ccattgcctg gagcaaccag      600
acaagcttca cctgccaaga tatcttcaaa gagaccaacg ccacctacc cagttcagac      660
gttccctgtg atgccacgtt gaccgagaaa agctttgaaa cagatatgaa cctgaacttt      720
caaaacctgt ct                                                                732
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<210> 242

<211> 283

<212> PRT

<213> Artificial Sequence

<220>

<223> KRAS TCR beta

<400> 242

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

```
Ser Trp Val Ala Leu Phe Leu Leu Gly Thr Ser Ser Ala Asn Ser Gly
20              25              30
```

```
Val Val Gln Ser Pro Arg Tyr Ile Ile Lys Gly Lys Gly Glu Arg Ser
35              40              45
```

```
Ile Leu Lys Cys Ile Pro Ile Ser Gly His Leu Ser Val Ala Trp Tyr
50              55              60
```

Gln Gln Thr Gln Gly Gln Glu Leu Lys Phe Phe Ile Gln His Tyr Asp
65 70 75 80

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

Gln Phe Asp Asp Tyr His Ser Glu Met Asn Met Ser Ala Leu Glu Leu
100 105 110

Glu Asp Ser Ala Val Tyr Phe Cys Ala Ser Ser Leu Thr Asp Pro Leu
115 120 125

Asp Ser Asp Tyr Thr Phe Gly Ser Gly Thr Arg Leu Leu Val Ile Glu
130 135 140

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

Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu Ala
165 170 175

Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
180 185 190

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

Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr
210 215 220

Phe Trp His Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe His
225 230 235 240

Gly Leu Ser Glu Glu Asp Lys Trp Pro Glu Gly Ser Pro Lys Pro Val
245 250 255

Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Ile
260 265 270

Thr Ser Ala Ser Tyr Gln Gln Gly Val Leu Ser
275 280

<210> 243
<211> 849
<212> DNA
<213> Artificial Sequence

<220>
<223> KRAS TCR beta

<400> 243
atgtctaaca ctgccttccc tgaccccgcc tggaacacca ccctgctatc ttgggttgct 60
ctcttttctcc tgggaacaag ttcagcaaatt tctgggggttg tccagtctcc aagatacata 120
atcaaaggaa agggagaaag gtccattcta aaatgtattc ccatctctgg acatctctct 180
gtggcctggg atcaacagac tcaggggcag gaactaaagt tcttcattca gcattatgat 240
aaaatggaga gagataaagg aaacctgccc agcagattct cagtccaaca gtttgatgac 300
tatcactctg agatgaacat gtagtccttg gagctagagg actctgccgt gtacttctgt 360
gccagctctc tcacagatcc gctagactcc gactacacct tcggctcagg gaccaggctt 420
ttggtaatag aggatctgag aaatgtgact ccaccaagg tctccttggt tgagccatca 480
aaagcagaga ttgcaaaca acaaaaggct accctcgtgt gcttggccag gggcttcttc 540
cctgaccacg tggagctgag ctggtgggtg aatggcaagg aggtccacag tgggggtctgc 600
acggaccctc aggcctacaa ggagagcaat tatagctact gcctgagcag ccgcctgagg 660
gtctctgcta ctttctggca caatcctcgc aaccatttcc gctgccaagt gcagttccat 720
gggctttcag aggaggacaa gtggccagag ggctcaccca aacctgtcac acagaacatc 780
agtgcagagg cctggggccg agcagactgt gggattacct cagcatccta tcaacaaggg 840
gtcttgtct 849

<210> 244
<211> 283
<212> PRT
<213> Artificial Sequence

<220>
<223> KRAS TCR beta

<400> 244

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

Ser Trp Val Ala Leu Phe Leu Leu Gly Thr Ser Ser Ala Asn Ser Gly
20 25 30

Val Val Gln Ser Pro Arg Tyr Ile Ile Lys Gly Lys Gly Glu Arg Ser
35 40 45

Ile Leu Lys Cys Ile Pro Ile Ser Gly His Leu Ser Val Ala Trp Tyr
50 55 60

Gln Gln Thr Gln Gly Gln Glu Leu Lys Phe Phe Ile Gln His Tyr Asp
65 70 75 80

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

Gln Phe Asp Asp Tyr His Ser Glu Met Asn Met Ser Ala Leu Glu Leu
100 105 110

Glu Asp Ser Ala Val Tyr Phe Cys Ala Ser Ser Leu Thr Asp Pro Leu
115 120 125

Asp Ser Asp Tyr Thr Phe Gly Ser Gly Thr Arg Leu Leu Val Ile Glu
130 135 140

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

Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr Leu Val Cys Leu Ala
165 170 175

Arg Gly Phe Phe Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly
180 185 190

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

Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr
210 215 220

Phe	Trp	His	Asn	Pro	Arg	Asn	His	Phe	Arg	Cys	Gln	Val	Gln	Phe	His
225					230					235					240

Gly	Leu	Ser	Glu	Glu	Asp	Lys	Trp	Pro	Glu	Gly	Ser	Pro	Lys	Pro	Val
			245						250					255	

Thr	Gln	Asn	Ile	Ser	Ala	Glu	Ala	Trp	Gly	Arg	Ala	Asp	Cys	Gly	Ile
		260						265					270		

Thr	Ser	Ala	Ser	Tyr	Gln	Gln	Gly	Val	Leu	Ser
	275						280			

<210> 245
 <211> 849
 <212> DNA
 <213> KRAS TCR beta

<400> 245	
atgtctaaca ctgccttccc tgaccccgcc tggaacacca ccctgctatc ttgggttgct	60
ctcttttctcc tgggaacaag ttcagcaaatt tctgggggttg tccagtctcc aagatacata	120
atcaaaggaa agggagaaag gtccattcta aaatgtattc ccatctctgg acatctctct	180
gtggcctggg atcaacagac tcaggggcag gaactaaagt tcttcattca gcattatgat	240
aaaatggaga gagataaagg aaacctgccc agcagattct cagtccaaca gtttgatgac	300
tatcactctg agatgaacat gaggccttg gagctagagg actctgccgt gtacttctgt	360
gccagctctc tcacagatcc gctagactcc gactacacct tcggctcagg gaccaggctt	420
ttggtaatag aggatctgag aaatgtgact ccaccaagg tctccttggt tgagccatca	480
aaagcagaga ttgcaaaca aaaaaaggct accctcgtgt gcttggccag gggcttcttc	540
cctgaccacg tggagctgag ctggtgggtg aatggcaagg aggtccacag tgggggtctgc	600
acggaccctc aggcctacaa ggagagcaat tatagctact gcctgagcag ccgcctgagg	660
gtctctgcta ctttctggca caatcctcgc aaccacttcc gctgccaagt gcagttccat	720
gggctttcag aggaggacaa gtggccagag ggctcaccca aacctgtcac acagaacatc	780
agtgcagagg cctggggccg agcagactgt gggattacct cagcatccta tcaacaaggg	840
gtcttgtct	849

<210> 246
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> KRAS TCRA

<400> 246

Met Lys Thr Val Thr Gly Pro Leu Phe Leu Cys Phe Trp Leu Gln Leu
1 5 10 15

Asn Cys Val Ser Arg Gly Glu Gln Val Glu Gln Arg Pro Pro His Leu
20 25 30

Ser Val Arg Glu Gly Asp Ser Ala Val Ile Thr Cys Thr Tyr Thr Asp
35 40 45

Pro Asn Ser Tyr Tyr Phe Phe Trp Tyr Lys Gln Glu Pro Gly Ala Ser
50 55 60

Leu Gln Leu Leu Met Lys Val Phe Ser Ser Thr Glu Ile Asn Glu Gly
65 70 75 80

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

Asn Leu Thr Ala Ala His Pro Gly Asp Ser Ala Ala Tyr Phe Cys Ala
100 105 110

Val Ser Gly Gly Thr Asn Ser Ala Gly Asn Lys Leu Thr Phe Gly Ile
115 120 125

Gly Thr Arg Val Leu Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala
130 135 140

Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu
145 150 155 160

Phe Thr Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser
165 170 175

Gly Thr Phe Ile Thr Asp Lys Cys Val Leu Asp Met Lys Ala Met Asp
180 185 190

Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr
195 200 205

Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp
210 215 220

Val Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met
225 230 235 240

Asn Leu Asn Phe Gln Asn Leu Ser
245

<210> 247
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> KRAS TCRA

<400> 247
atgaagacgg tgactggacc tttgttcctg tgcttctggc tgcagctgaa ctgtgtgagc 60
agaggcgagc aggtggagca gcgccctcct cacctgagtg tccgggaggg agacagtgcc 120
gttatcacct gcacctacac agaccctaac agttattact tcttctggta caagcaagag 180
ccggggggcaa gtcttcagtt gcttatgaag gttttctcaa gtacggaaat aaacgaagga 240
caaggattca ctgtcctact gaacaagaaa gacaaacgac tctctctgaa cctcacagct 300
gccccatcctg gggactcagc cgcgtacttc tgcgcagtca gtggagggac taacagtgca 360
gggaacaagc taacttttgg aattggaacc aggggtgctgg tcaggccaga catccagaac 420
ccagaacctg ctgtgtacca gttaaaagat cctcgggtctc aggacagcac cctctgcctg 480
ttcaccgact ttgactccca aatcaatgtg ccgaaaacca tggaatctgg aacgttcac 540
actgacaaat gtgtgctgga catgaaagct atggattcca agagcaatgg ggccattgcc 600
tggagcaacc agacaagctt cacctgccaa gatattctca aagagaccaa cgccacctac 660
cccagttcag acgttcctg tgatgccacg ttgaccgaga aaagctttga aacagatatg 720

aacctgaact ttcaaacct gtct

744

<210> 248
<211> 272
<212> PRT
<213> Artificial Sequence

<220>
<223> KRAS TCRb

<400> 248

Met Gly Cys Arg Leu Leu Ser Cys Val Ala Phe Cys Leu Leu Gly Ile
1 5 10 15

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
65 70 75 80

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

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
100 105 110

Ser Arg Asp Trp Gly Pro Ala Glu Gln Phe Phe Gly Pro Gly Thr Arg
115 120 125

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

Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr
145 150 155 160

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

165

170

175

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro
 180 185 190

Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu
 195 200 205

Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys
 210 215 220

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

Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg
 245 250 255

Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser
 260 265 270

<210> 249

<211> 816

<212> DNA

<213> Artificial Sequence

<220>

<223> KRAS TCRb

<400> 249

atgggctgta ggctcctaag ctgtgtggcc ttctgcctct tgggaatagg ccctttggag 60

acagctgttt tccagactcc aaactatcat gtcacacagg tgggaaatga agtgtctttc 120

aattgtaagc aaactctggg ccacgatact atgtattggg acaagcaaga ctctaagaaa 180

ttgctgaaga ttatgttttag ctacaataat aagcaactca ttgtaaacga aacagttcca 240

aggcgcttct cacctcagtc ttcagataaa gctcatttga atcttcgaat caagtctgta 300

gagccggagg actctgctgt gatatctctgt gccagcagtc gggactgggg gcctgctgag 360

cagttcttcg gaccagggac acgactcacc gtcctagagg atctgagaaa tgtgactcca 420

cccaaggctc cttgttttga gccatcaaaa gcagagattg caaacaacaa aaaggctacc 480

ctcgtgtgct tggccagggg cttcttcctt gaccacgtgg agctgagctg gtgggtgaat 540

ggcaaggagg tccacagtgg ggtctgcacg gaccctcagg cctacaagga gagcaattat 600
 agctactgcc tgagcagccg cctgagggtc tctgctacct tctggcaciaa tcctcgaaac 660
 cacttccgct gccaaagtga gttccatggg ctttcagagg aggacaagtg gccagagggc 720
 tcacccaaac ctgtcacaca gaacatcagt gcagaggcct ggggccgagc agactgtgga 780
 atcacttcag catcctatca tcaggggggtt ctgtct 816

<210> 250
 <211> 272
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> KRAS TCRb

<400> 250

Met Gly Cys Arg Leu Leu Ser Cys Val Ala Phe Cys Leu Leu Gly Ile
 1 5 10 15

Gly Pro Leu Glu Thr Ala Val Phe Gln Thr Pro Asn Tyr His Val Thr
 20 25 30

Gln Val Gly Asn Glu Val Ser Phe Asn Cys Lys Gln Thr Leu Gly His
 35 40 45

Asp Thr Met Tyr Trp Tyr Lys Gln Asp Ser Lys Lys Leu Leu Lys Ile
 50 55 60

Met Phe Ser Tyr Asn Asn Lys Gln Leu Ile Val Asn Glu Thr Val Pro
 65 70 75 80

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

Ile Lys Ser Val Glu Pro Glu Asp Ser Ala Val Tyr Leu Cys Ala Ser
 100 105 110

Ser Arg Asp Trp Gly Pro Ala Glu Gln Phe Phe Gly Pro Gly Thr Arg
 115 120 125

Leu Thr Val Leu Glu Asp Leu Arg Asn Val Thr Pro Pro Lys Val Ser

130

135

140

Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln Lys Ala Thr
 145 150 155 160

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

Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Cys Thr Asp Pro
 180 185 190

Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser Ser Arg Leu
 195 200 205

Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His Phe Arg Cys
 210 215 220

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

Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala Glu Ala Trp Gly Arg
 245 250 255

Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His Gln Gly Val Leu Ser
 260 265 270

<210> 251
 <211> 816
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> KRAS TCRb

<400> 251
 atgggctgta ggctcctaag ctgtgtggcc ttctgcctct tgggaatagg ccctttggag 60
 acagctgttt tccagactcc aaactatcat gtcacacagg tgggaaatga agtgtctttc 120
 aattgtaagc aaactctggg ccacgatact atgtattgggt acaagcaaga ctctaagaaa 180
 ttgctgaaga ttatgttttag ctacaataat aagcaactca ttgtaaacga aacagttcca 240
 aggcgcttct cacctcagtc ttcagataaa gctcatttga atcttcgaat caagtctgta 300

gagccggagg actctgctgt gtatctctgt gccagcagtc gggactgggg gcctgctgag 360
 cagttcttcg gaccagggac acgactcacc gtcctagagg atctgagaaa tgtgactcca 420
 cccaaggctc cttgtttga gccatcaaaa gcagagattg caaacaaca aaaggctacc 480
 ctcgtgtgct tggccagggg cttcttcct gaccacgtgg agctgagctg gtgggtgaat 540
 ggcaaggagg tccacagtgg ggtctgcacg gaccctcagg cctacaagga gagcaattat 600
 agctactgcc tgagcagccg cctgagggtc tctgctacct tctggcacia tcctcgaaac 660
 cacttccgct gccaagtga gttccatggg ctttcagagg aggacaagtg gccagagggc 720
 tcacccaaac ctgtcacaca gaacatcagt gcagaggcct ggggccgagc agactgtgga 780
 atcacttcag catcctatca tcaggggggtt ctgtct 816

<210> 252
 <211> 244
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCRA control

<400> 252

Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val Gln Ile
 1 5 10 15

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

Leu His Glu Gly Thr Asp Ser Ala Leu Arg Cys Asn Phe Thr Thr Thr
 35 40 45

Met Arg Ser Val Gln Trp Phe Arg Gln Asn Ser Arg Gly Ser Leu Ile
 50 55 60

Ser Leu Phe Tyr Leu Ala Ser Gly Thr Lys Glu Asn Gly Arg Leu Lys
 65 70 75 80

Ser Ala Phe Asp Ser Lys Glu Arg Arg Tyr Ser Thr Leu His Ile Arg
 85 90 95

Asp Ala Gln Leu Glu Asp Ser Gly Thr Tyr Phe Cys Ala Ala Asp Ser

100

105

110

Ser Asn Thr Gly Tyr Gln Asn Phe Tyr Phe Gly Lys Gly Thr Ser Leu
 115 120 125

Thr Val Ile Pro Asn Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu
 130 135 140

Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe
 145 150 155 160

Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile
 165 170 175

Thr Asp Lys Cys Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn
 180 185 190

Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile
 195 200 205

Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp
 210 215 220

Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe
 225 230 235 240

Gln Asn Leu Ser

<210> 253
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCRA control

<400> 253
 atgcagagga acctgggagc tgtgctgggg attctgtggg tgcagatttg ctgggtgaga 60
 ggggatcagg tggagcagag tccttcagcc ctgagcctcc acgagggaac cgattctgct 120
 ctgagatgca attttacgac caccatgagg agtgtgcagt gggtccgaca gaattccagg 180

ggagcctca tcagtttggt ctacttggtc tcaggaacaa aggagaatgg gaggctaaag 240
 tcagcatttg attctaagga gcggcgctac agcaccctgc acatcaggga tgcccagctg 300
 gaggactcag gcacttactt ctgtgctgct gactcttcga acacgggtta ccagaacttc 360
 tattttggga aaggaacaag ttgactgtc attcacaaca tccagaaccc agaactgct 420
 gtgtaccagt taaaagatcc tcggtctcag gacagcacc tctgcctggt caccgacttt 480
 gactcccaaa tcaatgtgcc gaaaaccatg gaatctggaa cgttcacac tgacaaatgt 540
 gtgctggaca tgaaagctat ggattccaag agcaatgggg ccattgcctg gagcaaccag 600
 acaagcttca cctgccaaga tatcttcaaa gagaccaacg ccacctacc cagttcagac 660
 gttccctgtg atgccacgtt gaccgagaaa agctttgaaa cagatatgaa cctgaacttt 720
 caaacctgt ct 732

<210> 254
 <211> 248
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCRA control

<400> 254

Met Lys Thr Val Thr Gly Pro Leu Phe Leu Cys Phe Trp Leu Gln Leu
 1 5 10 15

Asn Cys Val Ser Arg Gly Glu Gln Val Glu Gln Arg Pro Pro His Leu
 20 25 30

Ser Val Arg Glu Gly Asp Ser Ala Val Ile Thr Cys Thr Tyr Thr Asp
 35 40 45

Pro Asn Ser Tyr Tyr Phe Phe Trp Tyr Lys Gln Glu Pro Gly Ala Ser
 50 55 60

Leu Gln Leu Leu Met Lys Val Phe Ser Ser Thr Glu Ile Asn Glu Gly
 65 70 75 80

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

Asn Leu Thr Ala Ala His Pro Gly Asp Ser Ala Ala Tyr Phe Cys Ala
100 105 110

Val Ser Gly Gly Thr Asn Ser Ala Gly Asn Lys Leu Thr Phe Gly Ile
115 120 125

Gly Thr Arg Val Leu Val Arg Pro Asp Ile Gln Asn Pro Glu Pro Ala
130 135 140

Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu
145 150 155 160

Phe Thr Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser
165 170 175

Gly Thr Phe Ile Thr Asp Lys Cys Val Leu Asp Met Lys Ala Met Asp
180 185 190

Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr
195 200 205

Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp
210 215 220

Val Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met
225 230 235 240

Asn Leu Asn Phe Gln Asn Leu Ser
245

<210> 255
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> TCRa control

<400> 255
atgaagacgg tgactggacc ttgtttcctg tgcttctggc tgcagctgaa ctgtgtgagc 60
agaggcgagc aggtggagca gcgccctcct cacctgagtg tccgggaggg agacagtgcc 120

gttatcacct gcacctacac agaccctaac agttattact tcttctggta caagcaagag	180
ccggggggcaa gtcttcagtt gcttatgaag gttttctcaa gtacggaaat aaacgaagga	240
caaggattca ctgtcctact gaacaagaaa gacaaacgac tctctctgaa cctcacagct	300
gcccaccttg gggactcagc cgcgtacttc tgcgcagtca gtggaggagac taacagtgca	360
gggaacaagc taacttttgg aattggaacc aggggtgctgg tcaggccaga catccagaac	420
ccagaacctg ctgtgtacca gttaaaagat cctcgggtctc aggacagcac cctctgcctg	480
ttcaccgact ttgactccca aatcaatgtg ccgaaaacca tggaatctgg aacgttcac	540
actgacaaat gtgtgctgga catgaaagct atggattcca agagcaatgg ggccattgcc	600
tggagcaacc agacaagctt cacctgccaa gatattctca aagagaccaa cgccacctac	660
cccagttcag acgttccttg tgatgccacg ttgaccgaga aaagctttga aacagatatg	720
aacctgaact ttcaaaacct gtct	744

<210> 256
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> mH-Y-2Db peptide

<400> 256

Lys	Cys	Ser	Arg	Asn	Arg	Gln	Tyr	Leu
1				5				

<210> 257
 <211> 614
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H-Y TCR alpha and beta

<400> 257

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

Gly	Asn	Ser	Ala	Gln	Ser	Val	Asp	Gln	Pro	Asp	Ala	His	Val	Thr	Leu
			20					25					30		

Ser Glu Gly Ala Ser Leu Glu Leu Arg Cys Ser Tyr Ser Tyr Ser Ala
35 40 45

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

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

Gly Phe Glu Ala Glu Phe Arg Lys Ser Asn Ser Ser Phe Asn Leu Lys
85 90 95

Lys Ser Pro Ala His Trp Ser Asp Ser Ala Lys Tyr Phe Cys Ala Leu
100 105 110

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

Thr Lys Leu Thr Val Ser Ser Pro Asp Ile Gln Asn Pro Glu Pro Ala
130 135 140

Val Tyr Gln Leu Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu
145 150 155 160

Phe Thr Asp Phe Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser
165 170 175

Gly Thr Phe Ile Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp
180 185 190

Ser Lys Ser Asn Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr
195 200 205

Cys Gln Asp Ile Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp
210 215 220

Val Pro Cys Asp Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met
225 230 235 240

Asn Leu Asn Phe Gln Asn Leu Ser Val Met Gly Leu Arg Ile Leu Leu

245

250

255

Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser
 260 265 270

Ser Arg Ala Lys Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu
 275 280 285

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ser Asn Thr
 290 295 300

Ala Phe Pro Asp Pro Ala Trp Asn Thr Thr Leu Leu Ser Trp Val Ala
 305 310 315 320

Leu Phe Leu Leu Gly Thr Lys His Met Glu Ala Ala Val Thr Gln Ser
 325 330 335

Pro Arg Asn Lys Val Ala Val Thr Gly Gly Lys Val Thr Leu Ser Cys
 340 345 350

Asn Gln Thr Asn Asn His Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr
 355 360 365

Gly His Gly Leu Arg Leu Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr
 370 375 380

Glu Lys Gly Asp Ile Pro Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln
 385 390 395 400

Glu Asn Phe Ser Leu Ile Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser
 405 410 415

Val Tyr Phe Cys Ala Ser Gly Asp Asn Ser Ala Glu Thr Leu Tyr Phe
 420 425 430

Gly Pro Gly Thr Arg Leu Thr Val Leu Glu Asp Leu Arg Asn Val Thr
 435 440 445

Pro Pro Lys Val Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn
 450 455 460

Lys Gln Lys Ala Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp
465 470 475 480

His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly
485 490 495

Val Ser Thr Asp Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys
500 505 510

Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg
515 520 525

Asn His Phe Arg Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp
530 535 540

Lys Trp Pro Glu Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala
545 550 555 560

Glu Ala Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His
565 570 575

Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys
580 585 590

Ala Thr Leu Tyr Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met
595 600 605

Val Lys Lys Lys Asn Ser
610

<210> 258
<211> 1845
<212> DNA
<213> Artificial Sequence

<220>
<223> H-Y TCR alpha and beta

<400> 258
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caatctgtcg atcagccaga tgcacacgtt accctttccg aggggtgcgtc acttgaactg 120

aggtgttcct atagctactc agcagcccct tatctgtttt ggtacgtaca ataccaggg	180
cagagtctcc aatttctcct taaatatata accggggaca ctgtagtgaa ggggactaaa	240
ggttttgaag cagagtttag gaagagcaac agctccttca accttaagaa gtcacccgca	300
cactggtcag actccgcgaa atacttctgt gctctggaag ggcaagacca ggggtggaagt	360
gccaaattga tatttggtga gggactaaa ttgactgtta gctcaccaga catccagaac	420
ccagaacctg ctgtgtacca gttaaaagat cctcgggtctc aggacagcac cctctgcctg	480
ttcaccgact ttgactccca aatcaatgtg ccgaaaacca tggaatctgg aacgttcac	540
actgacaaaa ctgtgctgga catgaaagct atggattcca agagcaatgg ggccattgcc	600
tggagcaacc agacaagctt cacctgccaa gatattctta aagagaccaa cgccacctac	660
cccagttcag acgttccctg tgatgccacg ttgaccgaga aaagctttga aacagatatg	720
aacctaaact ttcaaaacct gtcagttatg ggactccgaa tcctcctgct gaaagtagcg	780
ggatttaacc tgctcatgac gctgaggctg tgggccagtc gggccaagcg gtccggatcc	840
ggagccacca acttcagcct gctgaagcag gccggcgacg tggaggagaa ccccgcccc	900
atgtctaata ctgcatttcc agatccggcc tggaatacta cactccttag ttgggttgcc	960
ctcttcctcc ttggcacgaa gcacatggaa gccgccgtca cccagagtcc gagaacaaaa	1020
gtagcgggtca ccggcggtaa ggtaacattg agttgtaacc aaacgaacaa ccataacaat	1080
atgtactggg atagacaaga cacaggccat ggcttgcgcc tgattcacta cagctatgga	1140
gcggggagta cggagaaggg tgatatcccc gatggctata aagcctctcg gcctagccag	1200
gagaatttta gtttgatcct ggagctcgca acccccagtc agactagcgt ctacttttgt	1260
gcctcaggcg acaatagtgc ggaaaccctt tacttcggcc ctgggacaag acttacagtt	1320
ctagaggatc tgagaaatgt gactccaccc aaggtctcct tgtttgagcc atcaaaagca	1380
gagattgcaa acaaacaaaa ggctaccctc gtgtgcttgg ccaggggctt cttccctgac	1440
cacgtggagc tgagctgggt ggtgaatggc aaggaggtcc acagtggggt cagcacggac	1500
cctcaggcct acaaggagag caattatagc tactgcctga gcagccgcct gaggggtctct	1560
gctaccttct ggcacaatcc tcgaaaccac ttccgctgcc aagtgcagtt ccatgggctt	1620
tcagaggagg acaagtggcc agagggtca cccaaacctg tcacacagaa catcagtgca	1680
gaggcctggg gccgagcaga ctgtggaatc acttcagcat cctatcatca gggggttctg	1740

tctgcaacca tcctctatga gatcctactg gggaaggcca ccctatatgc tgtgctggtc 1800
 agtggcctgg tgctgatggc catggtcaag aaaaaaatt cctag 1845

<210> 259
 <211> 619
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H-Y TCR alpha and beta

<400> 259

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

Gly Asn Ser Ala Gln Ser Val Asp Gln Pro Asp Ala His Val Thr Leu
 20 25 30

Ser Glu Gly Ala Ser Leu Glu Leu Arg Cys Ser Tyr Ser Tyr Ser Ala
 35 40 45

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

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

Gly Phe Glu Ala Glu Phe Arg Lys Ser Asn Ser Ser Phe Asn Leu Lys
 85 90 95

Lys Ser Pro Ala His Trp Ser Asp Ser Ala Lys Tyr Phe Cys Ala Leu
 100 105 110

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

Thr Lys Leu Thr Val Ser Ser Pro Tyr Ile Gln Asn Pro Asp Pro Ala
 130 135 140

Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu
 145 150 155 160

Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser
165 170 175

Asp Val Tyr Ile Thr Asp Lys Cys Val Leu Asp Met Arg Ser Met Asp
180 185 190

Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala
195 200 205

Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe
210 215 220

Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe
225 230 235 240

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

Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
260 265 270

Arg Leu Trp Ser Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
275 280 285

Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ser Asn Thr Ala
290 295 300

Phe Pro Asp Pro Ala Trp Asn Thr Thr Leu Leu Ser Trp Val Ala Leu
305 310 315 320

Phe Leu Leu Gly Thr Lys His Met Glu Ala Ala Val Thr Gln Ser Pro
325 330 335

Arg Asn Lys Val Ala Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn
340 345 350

Gln Thr Asn Asn His Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly
355 360 365

His Gly Leu Arg Leu Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu

370

375

380

Lys Gly Asp Ile Pro Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu
 385 390 395 400

Asn Phe Ser Leu Ile Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val
 405 410 415

Tyr Phe Cys Ala Ser Gly Asp Asn Ser Ala Glu Thr Leu Tyr Phe Gly
 420 425 430

Pro Gly Thr Arg Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro
 435 440 445

Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr
 450 455 460

Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His
 465 470 475 480

Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val
 485 490 495

Cys Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser
 500 505 510

Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln
 515 520 525

Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser
 530 535 540

Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile
 545 550 555 560

Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu
 565 570 575

Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu
 580 585 590

Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu
595 600 605

Met Ala Met Val Lys Arg Lys Asp Ser Arg Gly
610 615

<210> 260
<211> 1860
<212> DNA
<213> Artificial Sequence

<220>
<223> H-Y TCR alpha and beta

<400> 260
atgttccccg ttaccatatt gtcctgagt gctttcttca gtttgcgagg gaactctgcc 60
caatctgtcg atcagccaga tgcacacgtt accctttccg aggggtgcgtc acttgaactg 120
aggtgttcct atagctactc agcagcccct tatctgtttt ggtacgtaca ataccagagg 180
cagagtctcc aatttctcct taaatatata accggggaca ctgtagtgaa ggggactaaa 240
ggttttgaag cagagtttag gaagagcaac agctccttca accttaagaa gtcacccgca 300
cactggtcag actccgcgaa atacttctgt gctctggaag ggcaagacca ggggtggaagt 360
gccaaattga tatttggtga ggggtactaaa ttgactgtta gctcaccgta tatccagaac 420
cctgaccctg ccgtgtacca gctgagagac tctaaatcca gtgacaagtc tgtctgccta 480
ttcaccgatt ttgattctca aacaaatgtg tcacaaagta aggattctga tgtgtatatc 540
acagacaaat gtgtgctaga catgaggctc atggacttca agagcaacag tgctgtggcc 600
tggagcaaca aatctgactt tgcattgtgca aacgccttca acaacagcat tattccagaa 660
gacaccttct tccccagccc agaaagttcc tgtgatgtca agctggtcga gaaaagcttt 720
gaaacagata cgaacctaaa ctttcaaaac ctgtcagtga ttgggttccg aatcctcctc 780
ctgaaagtgg ccgggtttta tctgctcatg acgctgcggc tgtggtccag cggatccgga 840
gccaccaact tcagcctgct gaagcaggcc ggcgacgtgg aggagaaccc cggccccatg 900
tctaatactg catttccaga tccggcctgg aatactacac tccttagttg ggttgcctc 960
ttcctccttg gcacgaagca catggaagcc gccgtcacc agagtccgag aaacaaagta 1020
gcggtcaccg gcggtaaggt aacattgagt tgtaaccaa cgaacaacca taacaatatg 1080

tactggtata gacaagacac aggccatggc ttgcgcctga ttcactacag ctatggagcg	1140
gggagtacgg agaagggtga tattcccgat ggctataaag cctctcggcc tagccaggag	1200
aatttttagtt tgatcctgga gctcgcaacc cccagtcaga ctagcgtcta cttttgtgcc	1260
tcaggcgaca atagtgcgga aaccctttac ttcggccctg ggacaagact tacagttctg	1320
gaggacctga aaaacgtgtt cccacccgag gtcgctgtgt ttgagccatc agaagcagag	1380
atctcccaca cccaaaaggc cacactgggtg tgcctggcca caggcttcta ccccgaccac	1440
gtggagctga gctgggtgggt gaatgggaag gaggtgcaca gtgggggtctg cacagacccg	1500
cagccccctca aggagcagcc cgccctcaat gactccagat actgcctgag cagccgcctg	1560
agggtgtcgg ccaccttctg gcagaacccc cgcaaccact tccgctgtca agtccagttc	1620
tacgggctct cggagaatga cgagtggacc caggataggg ccaaacctgt caccagatc	1680
gtcagcgccg aggctgggg tagagcagac tgtggcttca cctccgagtc ttaccagcaa	1740
ggggtcctgt ctgccacat cctctatgag atcttgctag ggaaggccac cttgtatgcc	1800
gtgctggtca gtgccctcgt gctgatggcc atggtcaaga gaaaggattc cagaggctag	1860

<210> 261
 <211> 614
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> H-Y TCR alpha and beta

<400> 261

Met	Phe	Pro	Val	Thr	Ile	Leu	Leu	Leu	Ser	Ala	Phe	Phe	Ser	Leu	Arg
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Gly	Asn	Ser	Ala	Gln	Ser	Val	Asp	Gln	Pro	Asp	Ala	His	Val	Thr	Leu
			20					25					30		

Ser	Glu	Gly	Ala	Ser	Leu	Glu	Leu	Arg	Cys	Ser	Tyr	Ser	Tyr	Ser	Ala
		35					40					45			

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

Phe	Leu	Leu	Lys	Tyr	Ile	Thr	Gly	Asp	Thr	Val	Val	Lys	Gly	Thr	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65				70				75				80			
Gly	Phe	Glu	Ala	Glu 85	Phe	Arg	Lys	Ser	Asn 90	Ser	Ser	Phe	Asn	Leu 95	Lys
Lys	Ser	Pro	Ala 100	His	Trp	Ser	Asp	Ser 105	Ala	Lys	Tyr	Phe	Cys 110	Ala	Leu
Glu	Gly	Gln 115	Asp	Gln	Gly	Gly	Ser 120	Ala	Lys	Leu	Ile	Phe 125	Gly	Glu	Gly
Thr	Lys 130	Leu	Thr	Val	Ser	Ser 135	Pro	Asp	Ile	Gln	Asn 140	Pro	Glu	Pro	Ala
Val 145	Tyr	Gln	Leu	Lys	Asp 150	Pro	Arg	Ser	Gln	Asp 155	Ser	Thr	Leu	Cys	Leu 160
Phe	Thr	Asp	Phe	Asp 165	Ser	Gln	Ile	Asn	Val 170	Pro	Lys	Thr	Met	Glu 175	Ser
Gly	Thr	Phe 180	Ile	Thr	Asp	Lys	Thr	Val 185	Leu	Asp	Met	Lys	Ala 190	Met	Asp
Ser	Lys 195	Ser	Asn	Gly	Ala	Ile	Ala 200	Trp	Ser	Asn	Gln	Thr 205	Ser	Phe	Thr
Cys 210	Gln	Asp	Ile	Phe	Lys	Glu 215	Thr	Asn	Ala	Thr	Tyr 220	Pro	Ser	Ser	Asp
Val 225	Pro	Cys	Asp	Ala	Thr 230	Leu	Thr	Glu	Lys	Ser 235	Phe	Glu	Thr	Asp	Met 240
Asn	Leu	Asn	Phe	Gln 245	Asn	Leu	Ser	Val	Met 250	Gly	Leu	Arg	Ile	Leu 255	Leu
Leu	Lys	Val	Ala 260	Gly	Phe	Asn	Leu	Leu	Met 265	Thr	Leu	Arg	Leu	Trp	Ser
Ser	Arg 275	Ala	Lys	Arg	Ser	Gly	Ser 280	Gly	Ala	Thr	Asn 285	Phe	Ser	Leu	Leu

Lys Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ser Asn Thr
290 295 300

Ala Phe Pro Asp Pro Ala Trp Asn Thr Thr Leu Leu Ser Trp Val Ala
305 310 315 320

Leu Phe Leu Leu Gly Thr Lys His Met Glu Ala Ala Val Thr Gln Ser
325 330 335

Pro Arg Asn Lys Val Ala Val Thr Gly Gly Lys Val Thr Leu Ser Cys
340 345 350

Asn Gln Thr Asn Asn His Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr
355 360 365

Gly His Gly Leu Arg Leu Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr
370 375 380

Glu Lys Gly Asp Ile Pro Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln
385 390 395 400

Glu Asn Phe Ser Leu Ile Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser
405 410 415

Val Tyr Phe Cys Ala Ser Gly Asp Asn Ser Ala Glu Thr Leu Tyr Phe
420 425 430

Gly Pro Gly Thr Arg Leu Leu Val Leu Glu Asp Leu Arg Asn Val Thr
435 440 445

Pro Pro Lys Val Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn
450 455 460

Lys Gln Lys Ala Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp
465 470 475 480

His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly
485 490 495

Val Ser Thr Asp Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys

500

505

510

Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg
 515 520 525

Asn His Phe Arg Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp
 530 535 540

Lys Trp Pro Glu Gly Ser Pro Lys Pro Val Thr Gln Asn Ile Ser Ala
 545 550 555 560

Glu Ala Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr His
 565 570 575

Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys
 580 585 590

Ala Thr Leu Tyr Ala Val Leu Val Ser Gly Leu Val Leu Met Ala Met
 595 600 605

Val Lys Lys Lys Asn Ser
 610

<210> 262
 <211> 1845
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> H-Y TCR alpha and beta

<400> 262
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 aggtgttcct atagctactc agcagcccct tatctgtttt ggtacgtaca ataccaggg 180
 cagagtctcc aatttctcct taaatatata accgggggaca ctgtagtgaa ggggactaaa 240
 ggttttgaag cagagtttag gaagagcaac agctccttca accttaagaa gtcacccgca 300
 cactgggtcag actccgcaaa atacttctgt gctctggaag ggcaagacca gggtggaagt 360
 gccaaattga tatttggtga gggtactaaa ttgactgtta gtcaccaga catccagaac 420

ccagaacctg ctgtgtacca gttaaaagat cctcggctctc aggacagcac cctctgcctg	480
ttcaccgact ttgactccca aatcaatgtg ccgaaaacca tggaatctgg aacgttcac	540
actgacaaaa ctgtgctgga catgaaagct atggattcca agagcaatgg ggccattgcc	600
tggagcaacc agacaagctt cacctgccaa gatattcttca aagagaccaa cgccacctac	660
cccagttcag acgttccttg tgatgccacg ttgaccgaga aaagctttga aacagatatg	720
aacctaaact ttcaaaacct gtcagttatg ggactccgaa tcctcctgct gaaagtagcg	780
ggatttaacc tgctcatgac gctgaggctg tgggtccagtc gggccaagcg gtccggatcc	840
ggagccacca acttcagcct gctgaagcag gccggcgacg tggaggagaa ccccggtccc	900
atgtctaata ctgcatttcc agatccggcc tggaatacta cactccttag ttgggttgcc	960
ctcttcctcc ttggcacgaa gcacatggaa gccgccgtca cccagagtcc gagaaacaaa	1020
gtagcgggtca ccggcggtaa ggtaacattg agttgtaacc aaacgaacaa ccataacaat	1080
atgtactggg atagacaaga cacaggccat ggcttgcgcc tgattcacta cagctatgga	1140
gcggggagta cggagaaggg tgatattccc gatggctata aagcctctcg gcctagccag	1200
gagaatttta gtttgatcct ggagctcgca acccccagtc agactagcgt ctacttttgt	1260
gcctcaggcg acaatagtgc ggaaaccctt tacttcggcc ctgggacaag acttttggtt	1320
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gagattgcaa acaaacaaaa ggctaccctc gtgtgcttgg ccaggggctt cttccctgac	1440
cacgtggagc tgagctgggt ggtgaatggc aaggaggtcc acagtggggt cagcacggac	1500
cctcaggcct acaaggagag caattatagc tactgcctga gcagccgcct gagggctctt	1560
gctaccttct ggcacaatcc tcgaaaccac ttccgctgcc aagtgcagtt ccatgggctt	1620
tcagaggagg acaagtggcc agagggctca cccaaacctg tcacacagaa catcagtgca	1680
gaggcctggg gccgagcaga ctgtggaatc acttcagcat cctatcatca gggggttctg	1740
tctgcaacca tcctctatga gatcctactg gggaaggcca ccctatatgc tgtgctggtc	1800
agtggcctgg tgctgatggc catggtcaag aaaaaaatt cctag	1845

<210> 263
 <211> 619
 <212> PRT
 <213> Artificial Sequence

<220>

<223> H-Y TCR alpha and beta

<400> 263

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

Gly Asn Ser Ala Gln Ser Val Asp Gln Pro Asp Ala His Val Thr Leu
20 25 30

Ser Glu Gly Ala Ser Leu Glu Leu Arg Cys Ser Tyr Ser Tyr Ser Ala
35 40 45

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

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

Gly Phe Glu Ala Glu Phe Arg Lys Ser Asn Ser Ser Phe Asn Leu Lys
85 90 95

Lys Ser Pro Ala His Trp Ser Asp Ser Ala Lys Tyr Phe Cys Ala Leu
100 105 110

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

Thr Lys Leu Thr Val Ser Ser Pro Tyr Ile Gln Asn Pro Asp Pro Ala
130 135 140

Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu
145 150 155 160

Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser
165 170 175

Asp Val Tyr Ile Thr Asp Lys Cys Val Leu Asp Met Arg Ser Met Asp
180 185 190

Phe Lys Ser Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala

195

200

205

Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe
 210 215 220

Pro Ser Pro Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe
 225 230 235 240

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

Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu
 260 265 270

Arg Leu Trp Ser Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys
 275 280 285

Gln Ala Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ser Asn Thr Ala
 290 295 300

Phe Pro Asp Pro Ala Trp Asn Thr Thr Leu Leu Ser Trp Val Ala Leu
 305 310 315 320

Phe Leu Leu Gly Thr Lys His Met Glu Ala Ala Val Thr Gln Ser Pro
 325 330 335

Arg Asn Lys Val Ala Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn
 340 345 350

Gln Thr Asn Asn His Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly
 355 360 365

His Gly Leu Arg Leu Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu
 370 375 380

Lys Gly Asp Ile Pro Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu
 385 390 395 400

Asn Phe Ser Leu Ile Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val
 405 410 415

Tyr Phe Cys Ala Ser Gly Asp Asn Ser Ala Glu Thr Leu Tyr Phe Gly
420 425 430

Pro Gly Thr Arg Leu Leu Val Leu Glu Asp Leu Lys Asn Val Phe Pro
435 440 445

Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr
450 455 460

Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His
465 470 475 480

Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val
485 490 495

Cys Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser
500 505 510

Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln
515 520 525

Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser
530 535 540

Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile
545 550 555 560

Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu
565 570 575

Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu
580 585 590

Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu
595 600 605

Met Ala Met Val Lys Arg Lys Asp Ser Arg Gly
610 615

<210> 264

<211> 1860
<212> DNA
<213> Artificial Sequence

<220>
<223> H-Y TCR alpha and beta

<400> 264
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aggtgttcct atagctactc agcagcccct tatctgtttt ggtacgtaca ataccaggg 180
cagagtctcc aatttctcct taaatatata accggggaca ctgtagtga ggggactaaa 240
ggttttgaag cagagtttag gaagagcaac agctccttca accttaagaa gtcacccgca 300
cactggtcag actccgcgaa atacttctgt gctctggaag ggcaagacca ggggtggaagt 360
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cctgaccctg ccgtgtacca gctgagagac tctaaatcca gtgacaagtc tgtctgccta 480
ttcaccgatt ttgatttca aacaaatgtg tcacaaagta aggattctga tgtgtatatc 540
acagacaaat gtgtgctaga catgaggctt atggacttca agagcaacag tgctgtggcc 600
tggagcaaca aatctgactt tgcatgtgca aacgccttca acaacagcat tattccagaa 660
gacaccttct tccccagccc agaaagttcc tgtgatgtca agctggtcga gaaaagcttt 720
gaaacagata cgaacctaaa ctttcaaac ctgtcagtga ttgggttccg aatcctcctc 780
ctgaaagtgg ccgggtttta tctgctcatg acgctgcggc tgtggtccag cggatccgga 840
gccaccaact tcagcctgct gaagcaggcc ggcgacgtgg aggagaaccc cggcccatg 900
tctaatactg catttccaga tccggcctgg aatactacac tccttagttg ggttgccctc 960
ttcctccttg gcacgaagca catggaagcc gccgtcacc agagtccgag aaacaaagta 1020
gcggtcaccg gcggttaagg aacattgagt tgtaacaaa cgaacaacca taacaatatg 1080
tactggtata gacaagacac aggccatggc ttgctcctga ttactacag ctatggagcg 1140
gggagtacgg agaagggtga tattcccgat ggctataaag cctctcggcc tagccaggag 1200
aattttagtt tgatcctgga gctcgcaacc ccagtcaga ctagcgtcta cttttgtgcc 1260
tcaggcgaca atagtgcgga aaccctttac ttggccctg ggacaagact tttggttctg 1320
gaggacctga aaaacgtgtt cccacccgag gtcgtgtgt ttgagccatc agaagcagag 1380

atctcccaca cccaaaaggc cacactggtg tgcctggcca caggcttcta ccccgaccac	1440
gtggagctga gctggtgggt gaatgggaag gaggtgcaca gtgggggtctg cacagacccg	1500
cagccccctca aggagcagcc cgccctcaat gactccagat actgcctgag cagccgcctg	1560
agggtgtcgg ccaccttctg gcagaacccc cgcaaccact tccgctgtca agtccagttc	1620
tacgggctct cggagaatga cgagtggacc caggataggg ccaaacctgt caccagatc	1680
gtcagcgccg aggcttgggg tagagcagac tgtggcttca cctccgagtc ttaccagcaa	1740
ggggtcctgt ctgccacat cctctatgag atcttgctag ggaaggccac cttgtatgcc	1800
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<210> 265
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> NY-ESO-1

<400> 265

Ser	Leu	Leu	Met	Trp	Ile	Thr	Gln	Val
1					5			

<210> 266
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> HA-1(R) peptide

<400> 266

Val	Leu	Arg	Asp	Asp	Leu	Leu	Glu	Ala
1					5			

<210> 267
 <211> 607
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> NY-ESO-1 TCR alpha and beta

<400> 267

Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp
1 5 10 15

Val Ser Ser Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val
20 25 30

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

Ile Tyr Asn Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr
50 55 60

Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg
65 70 75 80

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

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

Pro Leu Tyr Gly Gly Ser Tyr Ile Pro Thr Phe Gly Arg Gly Thr Ser
115 120 125

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

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

Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr
165 170 175

Ile Thr Asp Lys Cys Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser
180 185 190

Asn Ser Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn
195 200 205

Ala Phe Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro

210

215

220

Glu Ser Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp
 225 230 235 240

Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu
 245 250 255

Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp
 260 265 270

Ser Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
 275 280 285

Asp Val Glu Glu Asn Pro Gly Pro Met Ser Ile Gly Leu Leu Cys Cys
 290 295 300

Ala Ala Leu Ser Leu Leu Trp Ala Gly Pro Val Asn Ala Gly Val Thr
 305 310 315 320

Gln Thr Pro Lys Phe Gln Val Leu Lys Thr Gly Gln Ser Met Thr Leu
 325 330 335

Gln Cys Ala Gln Asp Met Asn His Glu Tyr Met Ser Trp Tyr Arg Gln
 340 345 350

Asp Pro Gly Met Gly Leu Arg Leu Ile His Tyr Ser Val Gly Ala Gly
 355 360 365

Ile Thr Asp Gln Gly Glu Val Pro Asn Gly Tyr Asn Val Ser Arg Ser
 370 375 380

Thr Thr Glu Asp Phe Pro Leu Arg Leu Leu Ser Ala Ala Pro Ser Gln
 385 390 395 400

Thr Ser Val Tyr Phe Cys Ala Ser Ser Tyr Val Gly Asn Thr Gly Glu
 405 410 415

Leu Phe Phe Gly Glu Gly Ser Arg Leu Thr Val Leu Glu Asp Leu Lys
 420 425 430

Asn Val Phe Pro Pro Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu
435 440 445

Ile Ser His Thr Gln Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe
450 455 460

Tyr Pro Asp His Val Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val
465 470 475 480

His Ser Gly Val Cys Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala
485 490 495

Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala
500 505 510

Thr Phe Trp Gln Asn Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe
515 520 525

Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro
530 535 540

Val Thr Gln Ile Val Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly
545 550 555 560

Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu
565 570 575

Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser
580 585 590

Ala Leu Val Leu Met Ala Met Val Lys Arg Lys Asp Ser Arg Gly
595 600 605

<210> 268
<211> 1824
<212> DNA
<213> Artificial Sequence

<220>
<223> NY-ESO-1 TCR alpha and beta

<400> 268

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caggaggtga cgcagattcc tgcagctctg agtgtcccag aaggagaaaa cttggttctg	120
aactgcagtt tctactgatag cgctatttac aacctccagt ggtttaggca ggaccctggg	180
aaaggactca catctctgtt gcttattcag tcaagtcaga gagagcaaac aagtggaaga	240
cttaatgcct cgctggataa atcatcagga cgtagtactt tatacattgc agcttctcag	300
cctggtgact cagccaccta cctctgtgct gtgaggcccc tctacggagg aagctacata	360
cctacatttg gaagaggaac cagccttatt gttcatccgt atatccagaa ccctgaccct	420
gccgtgtacc agctgagaga ctctaaatcc agtgacaagt ctgtctgcct attcaccgat	480
tttgattctc aaacaaatgt gtcacaaagt aaggattctg atgtgtatat cacagacaaa	540
tgtgtgctag acatgaggtc tatggacttc aagagcaaca gtgctgtggc ctggagcaac	600
aaatctgact ttgcatgtgc aaacgccttc aacaacagca ttattccaga agacaccttc	660
ttccccagcc cagaaaagttc ctgtgatgtc aagctggtcg agaaaagctt tgaaacagat	720
acgaacctaa actttcaaaa cctgtcagtg attgggttcc gaatcctcct cctgaaagtg	780
gccgggttta atctgctcat gacgctgcgg ctgtgggtcca gcggatccgg agccaccaac	840
ttcagcctgc tgaagcaggc cggcgacgtg gaggagaacc ccggcccat gagcatcggc	900
ctcctgtgct gtgcagcctt gtctctcctg tgggcaggtc cagtgaatgc tgggtgcact	960
cagaccccaa aattccaggt cctgaagaca ggacagagca tgacactgca gtgtgcccag	1020
gatatgaacc atgaatacat gtcctggtat cgacaagacc caggcatggg gctgaggctg	1080
attcattact cagttggtgc tggatatcact gaccaaggag aagtcccaa tggctacaat	1140
gtctccagat caaccacaga ggatttcccg ctcaggctgc tgtcggctgc tccctcccag	1200
acatctgtgt acttctgtgc cagcagttac gtcgggaaca ccggggagct gttttttgga	1260
gaaggctcta ggctgaccgt actggaggac ctgaaaaacg tgttcccacc cgaggtcgct	1320
gtgtttgagc catcagaagc agagatctcc cacacccaaa aggccacact ggtgtgcctg	1380
gccacaggct tctaccccga ccacgtggag ctgagctggt ggggtgaatgg gaaggaggtg	1440
cacagtgggg tctgcacaga cccgcagccc ctcaaggagc agcccgcct caatgactcc	1500
agatactgcc tgagcagccg cctgagggtg tcggccacct tctggcagaa cccccgaac	1560
cacttccgct gtcaagtcca gttctacggg ctctcggaga atgacgagtg gaccaggat	1620

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agggccaaac ctgtcaccca gatcgtcagc gccgaggcct ggggtagagc agactgtggc      1680
ttcacctccg agtcttacca gcaaggggtc ctgtctgccca ccatactcta tgagatcttg      1740
ctagggaagg ccaccttgta tgccgtgctg gtcagtgccc tcgtgctgat ggccatggtc      1800
aagagaaagg attccagagg ctag                                              1824

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<210> 269
<211> 612
<212> PRT
<213> Artificial Sequence

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<220>
<223> KRAS TCR

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<400> 269

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Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val Gln Ile
1           5           10          15

```

```

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

```

```

Leu His Glu Gly Thr Asp Ser Ala Leu Arg Cys Asn Phe Thr Thr Thr
          35          40          45

```

```

Met Arg Ser Val Gln Trp Phe Arg Gln Asn Ser Arg Gly Ser Leu Ile
          50          55          60

```

```

Ser Leu Phe Tyr Leu Ala Ser Gly Thr Lys Glu Asn Gly Arg Leu Lys
65          70          75          80

```

```

Ser Ala Phe Asp Ser Lys Glu Arg Arg Tyr Ser Thr Leu His Ile Arg
          85          90          95

```

```

Asp Ala Gln Leu Glu Asp Ser Gly Thr Tyr Phe Cys Ala Ala Asp Ser
          100         105         110

```

```

Ser Asn Thr Gly Tyr Gln Asn Phe Tyr Phe Gly Lys Gly Thr Ser Leu
          115         120         125

```

```

Thr Val Ile Pro Asn Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu
          130         135         140

```

Lys Asp Pro Arg Ser Gln Asp Ser Thr Leu Cys Leu Phe Thr Asp Phe
145 150 155 160

Asp Ser Gln Ile Asn Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile
165 170 175

Thr Asp Lys Thr Val Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn
180 185 190

Gly Ala Ile Ala Trp Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile
195 200 205

Phe Lys Glu Thr Asn Ala Thr Tyr Pro Ser Ser Asp Val Pro Cys Asp
210 215 220

Ala Thr Leu Thr Glu Lys Ser Phe Glu Thr Asp Met Asn Leu Asn Phe
225 230 235 240

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

Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser Arg Ala Lys
260 265 270

Arg Ser Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly
275 280 285

Asp Val Glu Glu Asn Pro Gly Pro Met Ser Asn Thr Ala Phe Pro Asp
290 295 300

Pro Ala Trp Asn Thr Thr Leu Leu Ser Trp Val Ala Leu Phe Leu Leu
305 310 315 320

Gly Thr Ser Ser Ala Asn Ser Gly Val Val Gln Ser Pro Arg Tyr Ile
325 330 335

Ile Lys Gly Lys Gly Glu Arg Ser Ile Leu Lys Cys Ile Pro Ile Ser
340 345 350

Gly His Leu Ser Val Ala Trp Tyr Gln Gln Thr Gln Gly Gln Glu Leu

355

360

365

Lys Phe Phe Ile Gln His Tyr Asp Lys Met Glu Arg Asp Lys Gly Asn
 370 375 380

Leu Pro Ser Arg Phe Ser Val Gln Gln Phe Asp Asp Tyr His Ser Glu
 385 390 395 400

Met Asn Met Ser Ala Leu Glu Leu Glu Asp Ser Ala Val Tyr Phe Cys
 405 410 415

Ala Ser Ser Leu Thr Asp Pro Leu Asp Ser Asp Tyr Thr Phe Gly Ser
 420 425 430

Gly Thr Arg Leu Leu Val Ile Glu Asp Leu Arg Asn Val Thr Pro Pro
 435 440 445

Lys Val Ser Leu Phe Glu Pro Ser Lys Ala Glu Ile Ala Asn Lys Gln
 450 455 460

Lys Ala Thr Leu Val Cys Leu Ala Arg Gly Phe Phe Pro Asp His Val
 465 470 475 480

Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
 485 490 495

Thr Asp Pro Gln Ala Tyr Lys Glu Ser Asn Tyr Ser Tyr Cys Leu Ser
 500 505 510

Ser Arg Leu Arg Val Ser Ala Thr Phe Trp His Asn Pro Arg Asn His
 515 520 525

Phe Arg Cys Gln Val Gln Phe His Gly Leu Ser Glu Glu Asp Lys Trp
 530 535 540

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

Trp Gly Arg Ala Asp Cys Gly Ile Thr Ser Ala Ser Tyr Gln Gln Gly
 565 570 575

Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr
580 585 590

Leu Tyr Ala Val Leu Val Ser Thr Leu Val Val Met Ala Met Val Lys
595 600 605

Arg Lys Asn Ser
610

<210> 270
<211> 1839
<212> DNA
<213> Artificial Sequence

<220>
<223> KRAS TCR

<400> 270
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ctgagatgca attttacgac caccatgagg agtgtgcagt gggtccgaca gaattccagg 180
ggcagcctca tcagtttggt ctacttggct tcaggaacaa aggagaatgg gaggctaaag 240
tcagcatttg attctaagga gcggcgctac agcaccctgc acatcaggga tgcccagctg 300
gaggactcag gcacttactt ctgtgctgct gactcttcga acacgggtta ccagaacttc 360
tattttggga aaggaacaag tttgactgtc attccaaaca tccagaacc agaacctgct 420
gtgtaccagt taaaagatcc tcggtctcag gacagcacc tctgcctgtt caccgacttt 480
gactcccaaa tcaatgtgcc gaaaaccatg gaatctggaa cgttcatcac tgacaaaact 540
gtgctggaca tgaaagctat ggattccaag agcaatgggg ccattgcctg gagcaaccag 600
acaagcttca cctgccaaga tatcttcaaa gagaccaacg ccacctacc cagttcagac 660
gttcctgtg atgccacgtt gaccgagaaa agctttgaaa cagatatgaa cctgaacttt 720
caaaacctgt cagttatggg actccgaatc ctctgctga aagtagcggg atttaacctg 780
ctcatgacgc tgaggctgtg gtccagtcgg gccaaagcgt ccggatccgg agccaccaac 840
ttcagcctgc tgaagcaggc cggcgacgtg gaggagaacc ccggcccat gtctaact 900
gccttccctg accccgcctg gaacaccacc ctgctatctt gggttgctct ctttctcctg 960

ggaacaagtt cagcaaattc tggggttgtc cagtctccaa gatacataat caaaggaaag	1020
ggagaaaggt ccattctaaa atgtattccc atctctggac atctctctgt ggcctggtat	1080
caacagactc aggggcagga actaaagttc ttcattcagc attatgataa aatggagaga	1140
gataaaggaa acctgcccag cagattctca gtccaacagt ttgatgacta tcactctgag	1200
atgaacatga gtgccttgga gctagaggac tctgccgtgt acttctgtgc cagctctctc	1260
acagatccgc tagactccga ctacaccttc ggctcaggga ccaggctttt ggtaatagag	1320
gatctgagaa atgtgactcc acccaaggtc tccttgtttg agccatcaaa agcagagatt	1380
gcaaacaaac aaaaggctac cctcgtgtgc ttggccaggg gcttcttccc tgaccacgtg	1440
gagctgagct ggtgggtgaa tggcaaggag gtccacagtg gggtcagcac ggaccctcag	1500
gcctacaagg agagcaatta tagctactgc ctgagcagcc gcctgagggt ctctgctacc	1560
ttctggcaca atcctcgcaa ccacttccgc tgccaagtgc agttccatgg gctttcagag	1620
gaggacaagt ggccagaggg ctcacccaaa cctgtcacac agaacatcag tgcagaggcc	1680
tggggccgag cagactgtgg gattacctca gcacacctc aacaaggggt cttgtctgcc	1740
accatcctct atgagatcct gctagggaaa gccaccctgt atgctgtgct tgtcagtaca	1800
ctggtggtga tggctatggt caaaagaaag aattcatag	1839

<210> 271
 <211> 18
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> T2A self cleaving peptide

 <400> 271

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

Gly Pro

<210> 272
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>

<223> E2A self cleaving peptide

<400> 272

Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1 5 10 15

Asn Pro Gly Pro
20

<210> 273

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> F2A self cleaving peptide

<400> 273

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
1 5 10 15

Glu Ser Asn Pro Gly Pro
20

<210> 274

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> ITIM

<220>

<221> Z

<222> (1)..(1)

<223> Z is S, I V or L

<220>

<221> X

<222> (2)..(2)

<223> X is any amino acid

<220>

<221> X

<222> (4)..(5)

<223> X is any amino acid

<220>
<221> Z
<222> (6)..(6)
<223> Z is I, V or L

<400> 274

Glx Xaa Tyr Xaa Xaa Glx
1 5

<210> 275
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 ScFv

<400> 275

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu
115 120 125

Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys
130 135 140

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
145 150 155 160

Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser
165 170 175

Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile
180 185 190

Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln
195 200 205

Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
210 215 220

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
225 230 235 240

Ser Ser

<210> 276
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 ScFv

<400> 276
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gatggaactg ttaaactcct gatctaccat acatcaagat tacactcagg agtcccatca 180
aggttcagtg gcagtgggtc tggaacagat tattctctca ccattagcaa cctggagcaa 240
gaagatatcg ccacttactt ttgccaacag ggtaatacgc ttccgtacac gttcggaggg 300
gggaccaagc tggagatcac aggtggcggg ggctcgggcg gtggtgggtc gggtggcggc 360
ggatctgagg tgaaactgca ggagtcagga cctggcctgg tggcgccctc acagagcctg 420

tccgtcacat gcactgtctc aggggtctca ttacccgact atggtgtaag ctggattcgc	480
cagcctccac gaaaggggtct ggagtggctg ggagtaatat ggggtagtga aaccacatac	540
tataattcag ctctcaaadc cagactgacc atcatcaagg acaactccaa gagccaagtt	600
ttcttaaaaa tgaacagtct gcaaactgat gacacagcca ttactactg tgccaaacat	660
tattactacg gtggtagcta tgctatggac tactggggcc aaggaacctc agtcaccgtg	720
tcctca	726

<210> 277
 <211> 244
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 ScFv

<400> 277

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

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

Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	Gly	Thr	Val	Lys	Leu	Leu	Ile
	35					40					45				

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

Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Asn	Leu	Glu	Gln
65				70					75					80	

Glu	Asp	Ile	Ala	Thr	Tyr	Phe	Cys	Gln	Gln	Gly	Asn	Thr	Leu	Pro	Tyr
			85						90					95	

Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Thr	Gly	Gly	Gly	Gly	Ser
		100					105						110		

Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Glu	Val	Lys	Leu
		115				120						125			

Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val
130 135 140

Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp
145 150 155 160

Ile Arg Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp
165 170 175

Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr
180 185 190

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

Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr
210 215 220

Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val
225 230 235 240

Thr Val Ser Ser

<210> 278
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 ScFv

<400> 278
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gatggaactg ttaaactcct gatctaccat acatcaagat tacactcagg agtcccatca 180
aggttcagtg gcagtgggtc tggacacagat tattctctca ccattagcaa cctggagcaa 240
gaagatattg ccacttactt ttgccaacag ggtaatacgc ttccgtacac gttcggaggg 300
gggaccaagc tggagatcac aggcggagggt ggaagcggag ggggaggatc tggcggcgga 360

ggaagcggag gcgaggtgaa actgcaggag tcaggacctg gcctggtggc gccctcacag 420
 agcctgtccg tcacatgcac tgtctcaggg gtctcattac ccgactatgg tgtaagctgg 480
 attcgccagc ctccacgaaa gggctctggag tggctgggag taatatgggg tagtgaaacc 540
 acatactata attcagctct caaatccaga ctgaccatca tcaaggacaa ctccaagagc 600
 caagttttct taaaaatgaa cagtctgcaa actgatgaca cagccattta ctactgtgcc 660
 aaacattatt actacggtgg tagctatgct atggactact ggggccaagg aacctcagtc 720
 accgtgtcct ca 732

<210> 279
 <211> 509
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CD19 CAR

<400> 279

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45

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

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
 65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser
 100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu
115 120 125

Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys
130 135 140

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
145 150 155 160

Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser
165 170 175

Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile
180 185 190

Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln
195 200 205

Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
210 215 220

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
225 230 235 240

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
245 250 255

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
260 265 270

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
275 280 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
290 295 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305 310 315 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
325 330 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
340 345 350

Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
355 360 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
370 375 380

Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385 390 395 400

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

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
420 425 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
435 440 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
450 455 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465 470 475 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
485 490 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505

<210> 280
<211> 1527
<212> DNA
<213> Artificial Sequence

<220>
<223> CD19 CAR

<400> 280

gacatccaga tgacacagac tacatcctcc ctgtctgcct ctctgggaga cagagtcacc	60
atcagttgca gggcaagtca ggacattagt aaatatTTaa attggtatca gcagaaacca	120
gatggaactg ttaaactcct gatctaccat acatcaagat tacactcagg agtcccatca	180
aggttcagtg gcagtgggtc tggaacagat tatttctctca ccattagcaa cctggagcaa	240
gaagatattg ccacttactt ttgccaacag ggtaatacgc ttccgtacac gttcggaggg	300
gggaccaagc tggagatcac aggtggcggt ggctcgggcg gtggtgggtc gggTggcggc	360
ggatctgagg tgaaactgca ggagtcagga cctggcctgg tggcgccctc acagagcctg	420
tccgtcacat gcactgtctc aggggtctca ttacccgact atggtgtaag ctggattcgc	480
cagcctccac gaaaggtctt ggagtggctg ggagtaatat ggggtagtga aaccacatac	540
tataattcag ctctcaaatac cagactgacc atcatcaagg acaactcaa gagccaagtt	600
ttcttaaaaa tgaacagtct gcaaactgat gacacagcca ttactactg tgccaaacat	660
tattactacg gtggtagcta tgctatggac tactggggcc aaggaacctc agtcaccgtg	720
tcctcaacca cgacgccagc gccgcgacca ccaacaccgg cggccaccat cgcgtcgcag	780
cccctgtccc tgcgcccaga ggcgtgccgg ccagcggcgg ggggcgcagt gcacacgagg	840
gggctggact tcgcctgtga tttctgggtg ctggctcgtt tgggcggcgt gctggcctgc	900
tacagcctgc tggtgacagt ggccttcatc atcttttggg tgaggagcaa gcggagcaga	960
ctgctgcaca gcgactacat gaacatgacc ccccgagggc ctggccccac ccggaagcac	1020
taccagccct acgcccctcc cagggtattc gccgcctacc ggagcaaacg gggcagaaag	1080
aaactcctgt atatattcaa acaaccattt atgaggccag taaaaactac tcaagaggaa	1140
gatggctgta gctgccgatt tccagaagaa gaagaaggag gatgtgaact gagagtgaag	1200
ttcagcagga gcgcagacgc ccccgcttac aagcagggcc agaaccagct ctataacgag	1260
ctcaatctag gacgaagaga ggagtacgat gttttggaca agcgtagagg ccgggaccct	1320
gagatggggg gaaagccgag aaggaagaac cctcaggaag gcctgtacaa tgaactgcag	1380
aaagataaga tggcggaggc ctacagtgag attgggatga aaggcgagcg ccggaggggc	1440
aaggggcacg atggccttta ccagggactc agtacagcca ccaaggacac ctacgacgcc	1500
cttcacatgc aggccctgcc ccctcgc	1527

<210> 281
<211> 509
<212> PRT
<213> Artificial Sequence

<220>
<223> CD19 CAR

<400> 281

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

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

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr Gly Gly Gly Gly Ser
100 105 110

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Lys Leu Gln Glu
115 120 125

Ser Gly Pro Gly Leu Val Ala Pro Ser Gln Ser Leu Ser Val Thr Cys
130 135 140

Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly Val Ser Trp Ile Arg
145 150 155 160

Gln Pro Pro Arg Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Ser
165 170 175

Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser Arg Leu Thr Ile Ile
180 185 190

Lys Asp Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln
195 200 205

Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Tyr Tyr Gly
210 215 220

Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val
225 230 235 240

Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
245 250 255

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
260 265 270

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe
275 280 285

Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu
290 295 300

Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg
305 310 315 320

Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro
325 330 335

Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala
340 345 350

Tyr Arg Ser Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln
355 360 365

Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser
370 375 380

Cys Arg Phe Pro Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys
385 390 395 400

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

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
420 425 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
435 440 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
450 455 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465 470 475 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
485 490 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
500 505

<210> 282
<211> 246
<212> PRT
<213> CEA ScFv

<400> 282

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Phe
20 25 30

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

Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
50 55 60

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

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

<210> 283
 <211> 1542
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> CEA ScFv

<400> 283

caggtgcagc tgggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtt	60
tcctgcaagg cttctggata caccttcact gagtttggaa tgaactgggt gcgacaggcc	120
cctggacaag ggcttgagt gatgggatgg ataaacacca aaactggaga ggcaacatat	180
gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat	240
ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac	300
ttcgcttatt acgtggaggc tatggactac tggggccaag ggaccacggt caccgtctcc	360
tcaggcggag gtggaagcgg agggggagga tctggcggcg gaggaagcgg aggcgatatc	420
cagatgaccc agtctccatc ctccctgtct gcatctgtgg gagacagagt caccatcact	480
tgcaaggcca gtcagaatgt gggactaat gttgcctgggt atcagcagaa accagggaaa	540
gcacctaagc tcctgatcta ttcggcatcc taccgctaca gtggagtccc atcaaggttc	600
agtggcagt gatctgggac agatttcact ctcaccatca gcagtctgca acctgaagat	660
ttcgcaactt actactgtca ccaatattac acctatcctc tattcacgtt tggccagggc	720
accaagctcg agatcaagat ggacatgagg gtccccgctc agctcctggg gtcctgcta	780
ctctggctcc gaggtgccag atgtcaggtg cagctgggtgc aatctgggtc tgagttgaag	840
aagcctgggg cctcagtga ggtttcctgc aaggcttctg gatacacctt cactgagttt	900
ggaatgaact ggggtgcgaca ggcccctgga caagggttg agtggatggg atggataaac	960
acaaaaactg gagaggcaac atatgttgaa gagtttaagg gacggtttgt cttctccttg	1020
gacacctctg tcagcacggc atatctgcag atcagcagcc taaaggctga agacactgcc	1080
gtgtattact gtgcgagatg ggacttcgct tattacgtgg aggctatgga ctactggggc	1140
caagggacca cggtcacctg ctccctcaggc ggaggtggaa gcggaggggg aggatctggc	1200
ggcggaggaa gcggaggcga tatccagatg acccagtctc catcctccct gtctgcatct	1260
gtgggagaca gagtacccat cacttgcaag gccagtcaga atgtgggtac taatgttgcc	1320
tggtatcagc agaaaccagg gaaagcacct aagctcctga tctattcggc atcctaccgc	1380
tacagtggag tcccatcaag gttcagtggc agtggatctg ggacagattt cactctcacc	1440
atcagcagtc tgcaacctga agatttcgca acttactact gtcaccaata ttacacctat	1500
cctctattca cgtttggcca gggcaccaag ctcgagatca ag	1542

<210> 284
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA ScFv

<400> 284

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Phe
20 25 30

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

Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
50 55 60

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

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

Ala Arg Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr Trp Gly
100 105 110

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

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

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

Cys Lys Ala Ser Ala Ala Val Gly Thr Tyr Val Ala Trp Tyr Gln Gln
165 170 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg
180 185 190

Lys Arg Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
195 200 205

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

Tyr Cys His Gln Tyr Tyr Thr Tyr Pro Leu Phe Thr Phe Gly Gln Gly
225 230 235 240

Thr Lys Leu Glu Ile Lys
245

<210> 285
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<223> CEA ScFv

<400> 285
caggtgcagc tggtgcagtc tggcgccgaa gtgaagaaac ctggagctag tgtgaaggtg 60
tcctgcaagg ccagcggcta caccttcacc gagttcggca tgaactgggt ccgacaggct 120
ccaggccagg gcctcgaatg gatgggctgg atcaacacca agaccggcga ggccacctac 180
gtggaagagt tcaagggcag agtgaccttc accacggaca ccagcaccag caccgcctac 240
atggaactgc ggagcctgag aagcgacgac accgccgtgt actactgcgc cagatgggac 300
ttcgcttatt acgtggaagc catggactac tggggccagg gcaccaccgt gaccgtgtct 360
agcggcggag gtggaagcgg agggggagga tctggcggcg gaggaagcgg aggcgatatc 420
cagatgaccc agtctccatc ctccctgtct gcatctgtgg gagacagagt caccatcact 480
tgcaaggcca gtgcggctgt gggtagtat gttgcgtggt atcagcagaa accagggaaa 540
gcacctaagc tcctgatcta ttccggcatcc taccgcaaaa ggggagtccc atcaaggttc 600
agtggcagtg gatctgggac agatttcact ctccatca gcagtctgca acctgaagat 660
ttcgcaactt actactgtca ccaatattac acctatcctc tattcacgtt tggccagggc 720

<210> 286
 <211> 246
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA ScFv

<400> 286

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Phe
 20 25 30

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

Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe
 50 55 60

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

Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Trp Asp Phe Ala His Tyr Phe Gln Thr Met Asp Tyr Trp Gly
 100 105 110

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

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

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

Cys Lys Ala Ser Ala Ala Val Gly Thr Tyr Val Ala Trp Tyr Gln Gln

165

170

175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg
 180 185 190

Lys Arg Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 195 200 205

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

Tyr Cys His Gln Tyr Tyr Thr Tyr Pro Leu Phe Thr Phe Gly Gln Gly
 225 230 235 240

Thr Lys Leu Glu Ile Lys
 245

<210> 287
 <211> 738
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEA ScFv

<400> 287
 caggtgcagc tgggtgcaatc tgggtctgag ttgaagaagc ctggggcctc agtgaaggtt 60
 tcctgcaagg cttctggata caccttcact gagtttggaa tgaactgggt gcgacaggcc 120
 cctggacaag ggcttgagt gatgggatgg ataaacacca aaactggaga ggcaacatat 180
 gttgaagagt ttaagggacg gtttgtcttc tccttggaca cctctgtcag cacggcatat 240
 ctgcagatca gcagcctaaa ggctgaagac actgccgtgt attactgtgc gagatgggac 300
 tttgctcatt actttcagac tatggactac tggggccaag ggaccacggt caccgtctcc 360
 tcaggcggag gtggaagcgg agggggagga tctggcggcg gaggaagcgg aggcgatatc 420
 cagatgaccc agtctccatc ctccctgtct gcatctgtgg gagacagagt caccatcact 480
 tgcaaggcca gtgcggctgt gggtacgtat gttgcgtgggt atcagcagaa accaggga 540
 gcacctaagc tcctgatcta ttcggcatcc taccgcaaaa ggggagtccc atcaaggttc 600
 agtggcagt gatctgggac agatttcact ctcacatca gcagtctgca acctgaagat 660

ttcgcaactt actactgtca ccaatattac acctatcctc tattcacgtt tggccagggc 720
 accaagctcg agatcaag 738

<210> 288
 <211> 535
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA CAR

<400> 288

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
 1 5 10 15

Leu Arg Gly Ala Arg Cys Gln Val Gln Leu Val Gln Ser Gly Ser Glu
 20 25 30

Leu Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
 35 40 45

Tyr Thr Phe Thr Glu Phe Gly Met Asn Trp Val Arg Gln Ala Pro Gly
 50 55 60

Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala
 65 70 75 80

Thr Tyr Val Glu Glu Phe Lys Gly Arg Phe Val Phe Ser Leu Asp Thr
 85 90 95

Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp
 100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Trp Asp Phe Ala Tyr Tyr Val Glu
 115 120 125

Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
 130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 145 150 155 160

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
165 170 175

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn
180 185 190

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
195 200 205

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
225 230 235 240

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Tyr Thr Tyr Pro Leu
245 250 255

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro
260 265 270

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
275 280 285

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
290 295 300

Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val Val
305 310 315 320

Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile
325 330 335

Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr
340 345 350

Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln
355 360 365

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

370

375

380

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

Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu
 405 410 415

Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp
 420 425 430

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

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
 450 455 460

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
 465 470 475 480

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
 485 490 495

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
 500 505 510

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
 515 520 525

Met Gln Ala Leu Pro Pro Arg
 530 535

<210> 289
 <211> 1608
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CEA CAR

<400> 289
 atggacatga ggggtccccgc tcagctcctg gggctcctgc tactctggct ccgaggtgcc

agatgtcagg tgcagctggt gcaatctggg tctgagttga agaagcctgg ggcctcagtg	120
aaggttttcct gcaaggcttc tggatacacc ttcactgagt ttggaatgaa ctgggtgcga	180
caggcccctg gacaagggct tgagtggatg ggatggataa acacaaaaac tggagaggca	240
acatatgttg aagagtttaa gggacggttt gtcttctcct tggacacctc tgtcagcacg	300
gcatatctgc agatcagcag cctaaaggct gaagacactg ccgtgtatta ctgtgcgaga	360
tgggacttcg cttattacgt ggaggctatg gactactggg gccaaaggac cacggtcacc	420
gtctcctcag gcggagggtg aagcggaggg ggaggatctg gcggcggagg aagcggaggc	480
gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc	540
atcacttgca aggccagtca gaatgtgggt actaatgttg cctggtatca gcagaaacca	600
gggaaagcac ctaagctcct gatctattcg gcatcctacc gctacagtgg agtcccatca	660
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	720
gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc	780
cagggcacca agctcgagat caagacaacg acgccagctc cccgcccgcc aacccttgca	840
cctacgattg catcacaacc gctgtccctg cggcctgaag cttgtcgccc agccgcaggt	900
ggcgccgtac atacacgggg gctggatttt gcctgtgatt tctgggtgct ggtcgtttgtg	960
ggcggcgtgc tggcctgcta cagcctgctg gtgacagtgg ctttcatcat cttttgggtg	1020
aggagcaagc ggagtcgact gctgcacagc gactacatga acatgacccc ccggaggcct	1080
ggccccaccc ggaagcacta ccagccctac gccctccca gggatttcgc cgcctaccgg	1140
agcaaacggg gcagaaagaa actcctgtat atattcaaac aaccatttat gaggccagta	1200
caaactactc aagaggaaga tggctgtagc tgccgatttc cagaagaaga agaaggagga	1260
tgtgaactga gagtgaagtt cagcaggagc gcagacgccc ccgcgtacaa gcagggccag	1320
aaccagctct ataacgagct caatctagga cgaagagagg agtacgatgt tttggacaag	1380
cgtagaggcc gggaccctga gatgggggga aagccgagaa ggaagaaccc tcaggaaggc	1440
ctgtacaatg aactgcagaa agataagatg gcggaggcct acagtgagat tgggatgaaa	1500
ggcgagcgcc ggagggggcaa ggggcacgat ggcctttacc agggactcag tacagccacc	1560
aaggacacct acgacgccct tcacatgcag gccctgcccc ctcgctag	1608

<211> 537
<212> PRT
<213> CEA CAR

<400> 290

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu
20 25 30

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
35 40 45

Tyr Thr Phe Thr Glu Phe Gly Met Asn Trp Val Arg Gln Ala Pro Gly
50 55 60

Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala
65 70 75 80

Thr Tyr Val Glu Glu Phe Lys Gly Arg Val Thr Phe Thr Thr Asp Thr
85 90 95

Ser Thr Ser Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Trp Asp Phe Ala Tyr Tyr Val Glu
115 120 125

Ala Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
165 170 175

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Ala Ala Val Gly Thr Tyr
180 185 190

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
195 200 205

Tyr Ser Ala Ser Tyr Arg Lys Arg Gly Val Pro Ser Arg Phe Ser Gly
210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
225 230 235 240

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Tyr Thr Tyr Pro Leu
245 250 255

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Thr Thr
260 265 270

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
275 280 285

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
290 295 300

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val
305 310 315 320

Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
325 330 335

Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
340 345 350

Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
355 360 365

Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys
370 375 380

Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg
385 390 395 400

Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro
405 410 415

Glu Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser
420 425 430

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

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
450 455 460

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
465 470 475 480

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
485 490 495

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
500 505 510

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
515 520 525

Leu His Met Gln Ala Leu Pro Pro Arg
530 535

<210> 291
<211> 1614
<212> DNA
<213> Artificial Sequence

<220>
<223> CEA CAR

<400> 291
atggacatga gggccccgc tcagctcctg gggctcctgc tactctggct ccgaggtgcc 60
agatgtcagg tgcagctggt gcagtctggc gccgaagtga agaaacctgg agctagtgtg 120
aaggtgtcct gcaaggccag cggctacacc ttcaccgagt tcggcatgaa ctgggtccga 180
caggctccag gccagggcct cgaatggatg ggctggatca acaccaagac cggcgaggcc 240
acctacgtgg aagagttcaa gggcagagtg accttcacca cggacaccag caccagcacc 300
gcctacatgg aactgcggag cctgagaagc gacgacaccg ccgtgtacta ctgcgccaga 360

tgggacttcg cttattacgt ggaagccatg gactactggg gccagggcac caccgtgacc	420
gtgtctagcg gcggaggtgg aagcggaggg ggaggatctg gcggcggagg aagcggaggg	480
gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc	540
atcacttgca aggccagtc ggctgtgggt acgtatgttg cgtggtatca gcagaaacca	600
gggaaagcac ctaagctcct gatctattcg gcacacctacc gcaaaagggg agtcccatca	660
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	720
gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc	780
cagggcacca agctcgagat caagcgtacg acaacgacgc cagctccccg cccgccaacc	840
cctgcaccta cgattgcatc acaaccgctg tccctgcggc ctgaagcttg tcgcccagcc	900
gcaggtggcg ccgtacatac acgggggctg gatcttgctt gtgatttctg ggtgctggtc	960
gttggtggcg gcgtgctggc ctgctacagc ctgctggtga cagtggcctt catcatcttt	1020
tgggtgagga gcaagcggag tcgactgctg cacagcgact acatgaacat gacccccgg	1080
aggcctggcc ccacccggaa gcactaccag ccctacgccc ctcccaggga tttcgccgcc	1140
taccggagca aacggggcag aaagaaactc ctgtatatat tcaaacaacc atttatgagg	1200
ccagtacaaa ctactcaaga ggaagatggc tgtagctgcc gatttccaga agaagaagaa	1260
ggaggatgtg aactgagagt gaagttcagc aggagcgagc acgccccgc gtacaagcag	1320
ggccagaacc agctctataa cgagctcaat ctaggacgaa gagaggagta cgatgttttg	1380
gacaagcgta gaggccggga ccctgagatg gggggaaagc cgagaaggaa gaaccctcag	1440
gaaggcctgt acaatgaact gcagaaagat aagatggcgg aggcctacag tgagattggg	1500
atgaaaggcg agcgccggag gggcaagggg cacgatggcc tttaccaggg actcagtaca	1560
gccaccaagg acacctacga cgcccttcac atgcaggccc tgccccctcg ctag	1614

<210> 292
 <211> 536
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA CAR

<400> 292

Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
1 5 10 15

Leu Arg Gly Ala Arg Cys Gln Val Gln Leu Val Gln Ser Gly Ser Glu
20 25 30

Leu Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
35 40 45

Tyr Thr Phe Thr Glu Phe Gly Met Asn Trp Val Arg Gln Ala Pro Gly
50 55 60

Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Lys Thr Gly Glu Ala
65 70 75 80

Thr Tyr Val Glu Glu Phe Lys Gly Arg Phe Val Phe Ser Leu Asp Thr
85 90 95

Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp
100 105 110

Thr Ala Val Tyr Tyr Cys Ala Arg Trp Asp Phe Ala His Tyr Phe Gln
115 120 125

Thr Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
145 150 155 160

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
165 170 175

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Ala Ala Val Gly Thr Tyr
180 185 190

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
195 200 205

Tyr Ser Ala Ser Tyr Arg Lys Arg Gly Val Pro Ser Arg Phe Ser Gly
210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
225 230 235 240

Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr Tyr Thr Tyr Pro Leu
245 250 255

Phe Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Thr Thr
260 265 270

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
275 280 285

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

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Phe Trp Val Leu Val Val
305 310 315 320

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe
325 330 335

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp
340 345 350

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr
355 360 365

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser Lys Arg
370 375 380

Gly Arg Lys Lys Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro
385 390 395 400

Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu
405 410 415

Glu Glu Glu Gly Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala
420 425 430

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

Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly
450 455 460

Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu
465 470 475 480

Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser
485 490 495

Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly
500 505 510

Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu
515 520 525

His Met Gln Ala Leu Pro Pro Arg
530 535

<210> 293
<211> 1611
<212> DNA
<213> Artificial Sequence

<220>
<223> CEA CAR

<400> 293
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agatgtcagg tgcagctggg gcaatctggg tctgagttga agaagcctgg ggcctcagtg 120
aaggtttcct gcaaggcttc tggatacacc ttactgagt ttggaatgaa ctgggtgcga 180
caggcccctg gacaagggtc tgagtggatg ggatggataa acacaaaac tggagaggca 240
acatatgttg aagagtttaa gggacgggtt gtcttctcct tggacacctc tgtcagcacg 300
gcatatctgc agatcagcag cctaaaggct gaagacactg ccgtgtatta ctgtgcgaga 360
tgggactttg ctattactt tcagactatg gactactggg gccaaaggac cacggtcacc 420
gtctcctcag gcggaggtgg aagcggaggg ggaggatctg gcggcggagg aagcggaggc 480
gatatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtgggaga cagagtcacc 540

atcacttgca aggccagtgc ggctgtgggt acgtatgttg cgtggtatca gcagaaacca	600
gggaaagcac ctaagctcct gatctattcg gcacccctacc gcaaaagggg agtcccatca	660
aggttcagtgc gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	720
gaagatttcg caacttacta ctgtcaccaa tattacacct atcctctatt cacgtttggc	780
cagggcacca agctcgagat caagcgtaca acgacgccag ctccccgccc gccaaaccct	840
gcacctacga ttgcatcaca accgctgtcc ctgcggcctg aagcttgctg cccagccgca	900
ggtggcgccg tacatacacg ggggctggat tttgcctgtg atttctgggt gctggtcgtt	960
gtgggcgccg tgctggcctg ctacagcctg ctggtgacag tggccttcat catcttttgg	1020
gtgaggagca agcggagtgc actgctgcac agcgactaca tgaacatgac cccccggagg	1080
cctggcccca cccggaagca ctaccagccc tacgcccctc ccagggattt cgccgcctac	1140
cggagcaaac ggggcagaaa gaaactcctg tatatatattca aacaaccatt tatgaggcca	1200
gtacaaaacta ctcaagagga agatggctgt agctgccgat ttccagaaga agaagaagga	1260
ggatgtgaac tgagagtga gttcagcagg agcgcagacg cccccgcgta caagcagggc	1320
cagaaccagc tctataacga gctcaatcta ggacgaagag aggagtacga tgttttggac	1380
aagcgtagag gccgggaccc tgagatgggg ggaaagccga gaaggaagaa ccctcaggaa	1440
ggcctgtaca atgaactgca gaaagataag atggcggagg cctacagtga gattgggatg	1500
aaaggcgagc gccggagggg caaggggcac gatggccttt accagggact cagtacagcc	1560
accaaggaca cctacgacgc ccttcacatg caggccctgc cccctcgcta g	1611

<210> 294
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> CEA CDR-H1

<400> 294

Glu	Phe	Gly	Met	Asn
1				5

<210> 295
 <211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> CEA CDR-H2

<400> 295

Trp Ile Asn Thr Lys Thr Gly Glu Ala Thr Tyr Val Glu Glu Phe Lys
1 5 10 15

Gly

<210> 296
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA CDR-H3

<400> 296

Trp Asp Phe Ala Tyr Tyr Val Glu Ala Met Asp Tyr
1 5 10

<210> 297
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA CDR-H3

<400> 297

Trp Asp Phe Ala His Tyr Phe Gln Thr Met Asp Tyr
1 5 10

<210> 298
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA CDR-L1

<400> 298

Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala
1 5 10

<210> 299
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA CDR-L1

<400> 299

Lys Ala Ser Ala Ala Val Gly Thr Tyr Val Ala
1 5 10

<210> 300
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA CDR-L2

<400> 300

Ser Ala Ser Tyr Arg Tyr Ser
1 5

<210> 301
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA CDR-L2

<400> 301

Ser Ala Ser Tyr Arg Lys Arg
1 5

<210> 302
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> CEA CDR-L3

<400> 302

His Gln Tyr Tyr Thr Tyr Pro Leu Phe Thr
1 5 10

<210> 303

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> LB-CYBA-1Y peptide

<220>

<221> X

<222> (10)..(10)

<223> X is Y or H

<400> 303

Ser Thr Met Glu Arg Trp Gly Gln Lys Xaa
1 5 10

<210> 304

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> LB-OAS1-1R

<220>

<221> X

<222> (7)..(7)

<223> X is R or T

<400> 304

Glu Thr Asp Asp Pro Arg Xaa Tyr Gln Lys Tyr
1 5 10

<210> 305

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> HA-2 peptide

<220>
<221> X
<222> (9)..(9)
<223> X is V or M

<400> 305

Tyr Ile Gly Glu Val Leu Val Ser Xaa
1 5

<210> 306
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HA-8 peptide

<220>
<221> X
<222> (1)..(1)
<223> X is R or P

<400> 306

Xaa Thr Leu Asp Lys Val Leu Glu Val
1 5

<210> 307
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HA-3 peptide

<220>
<221> X
<222> (2)..(2)
<223> X is T or M

<400> 307

Val Xaa Glu Pro Gly Thr Ala Gln Tyr
1 5

<210> 308
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> HwA11-S peptide

<220>
<221> X
<222> (6)..(6)
<223> X is S or T

<400> 308

Cys Ile Pro Pro Asp Xaa Leu Leu Phe Pro Ala
1 5 10

<210> 309
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LB-ADIR-1F peptide

<220>
<221> X
<222> (9)..(9)
<223> X is F or S

<400> 309

Ser Val Ala Pro Ala Leu Ala Leu Xaa Pro Ala
1 5 10

<210> 310
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LB-HIVEP1-1S peptide

<220>
<221> X
<222> (6)..(6)
<223> X is S or N

<400> 310

Ser Leu Pro Lys His Xaa Val Thr Ile
1 5

<210> 311
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LB-NISCH-1A peptide

<220>
<221> X
<222> (7)..(7)
<223> X is A or V

<400> 311

Ala Leu Ala Pro Ala Pro Xaa Glu Val
1 5

<210> 312
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LB-SSR1-1S peptide

<220>
<221> X
<222> (1)..(1)
<223> X is S or L

<400> 312

Xaa Leu Ala Val Ala Gln Asp Leu Thr
1 5

<210> 313
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> LB-WNK1-1I peptide

<220>

<221> X
<222> (7)..(7)
<223> X is I or M

<400> 313

Arg Thr Leu Ser Pro Glu Xaa Ile Thr Val
1 5 10

<210> 314
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> T4A peptide

<220>
<221> X
<222> (10)..(10)
<223> X is A or E

<400> 314

Gly Leu Tyr Thr Tyr Trp Ser Ala Gly Xaa
1 5 10

<210> 315
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> UTA2-1 peptide

<220>
<221> X
<222> (3)..(3)
<223> X is L or P

<400> 315

Gln Leu Xaa Asn Ser Val Leu Thr Leu
1 5

<210> 316
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LB-CLYBL-1Y peptide

<220>
<221> X
<222> (5)..(5)
<223> X is Y or D

<400> 316

Ser Leu Ala Ala Xaa Ile Pro Arg Leu
1 5

<210> 317
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> TRIM22 peptide

<220>
<221> X
<222> (7)..(7)
<223> X is C or R

<400> 317

Met Ala Val Pro Pro Cys Xaa Ile Gly Val
1 5 10

<210> 318
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> PARP10-1L peptide

<220>
<221> X
<222> (3)..(3)
<223> X is L or P

<400> 318

Gly Leu Xaa Gly Gln Glu Gly Leu Val Glu Ile
1 5 10

<210> 319
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FAM119A-1T peptide

<220>
<221> X
<222> (8)..(8)
<223> X is T or I

<400> 319

Ala Met Leu Glu Arg Gln Phe Xaa Val
1 5

<210> 320
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> GLRX3-1S peptide

<220>
<221> X
<222> (3)..(3)
<223> X is S or P

<400> 320

Phe Leu Xaa Ser Ala Asn Glu His Leu
1 5

<210> 321
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HNF4G-1M peptide

<220>
<221> X
<222> (2)..(2)

<223> X is M or I

<400> 321

Met Xaa Tyr Lys Asp Ile Leu Leu Leu
1 5

<210> 322

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> HMMR-1V peptide

<220>

<221> X

<222> (6)..(6)

<223> X is V or A

<400> 322

Ser Leu Gln Glu Lys Xaa Ala Lys Ala
1 5

<210> 323

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> BCL2A1 peptide

<220>

<221> X

<222> (4)..(4)

<223> X is N or K

<400> 323

Val Leu Gln Xaa Val Ala Phe Ser Val
1 5

<210> 324

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> CDC26-1F peptide

<220>

<221> X

<222> (1)..(1)

<223> X is F or S

<400> 324

Xaa	Val	Ala	Gly	Thr	Gln	Glu	Val	Phe	Val
1				5					10

<210> 325

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> APOBEC3F-1S/A peptide

<220>

<221> X

<222> (3)..(3)

<223> X is S or A

<400> 325

Phe	Leu	Xaa	Glu	His	Pro	Asn	Val	Thr	Leu
1				5					10

<210> 326

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> LB-PRCP-1D peptide

<220>

<221> X

<222> (8)..(8)

<223> X is D or E

<400> 326

Phe	Met	Trp	Asp	Val	Ala	Glu	Xaa	Leu
1				5				

<210> 327
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LB-PRCP-1D peptide

<220>
<221> X
<222> (8)..(8)
<223> X is D or E

<400> 327

Phe Met Trp Asp Val Ala Glu Xaa Leu Lys Ala
1 5 10

<210> 328
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LB-CCL4-1T peptide

<220>
<221> X
<222> (7)..(7)
<223> X is T or S

<400> 328

Cys Ala Asp Pro Ser Glu Xaa Trp Val
1 5

<210> 329
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LB-NCAPD3-1Q peptide

<220>
<221> X
<222> (3)..(3)
<223> X is Q or R

<400> 329

Trp Leu Xaa Gly Val Val Pro Val Val
1 5

<210> 330

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> LB-NDC80-1P peptide

<220>

<221> X

<222> (7)..(7)

<223> X is P or A

<400> 330

His Leu Glu Glu Gln Ile Xaa Lys Val
1 5

<210> 331

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> LB-TTK-1D peptide

<220>

<221> X

<222> (4)..(4)

<223> X is D or E

<400> 331

Arg Leu His Xaa Gly Arg Val Phe Val
1 5

<210> 332

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> WDR27-1L peptide

<220>
<221> X
<222> (2)..(2)
<223> X is L or P

<400> 332

Ser Xaa Asp Asp His Val Val Ala Val
1 5

<210> 333
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> MIIP peptide

<220>
<221> X
<222> (8)..(8)
<223> X is K or E

<400> 333

Ser Glu Glu Ser Ala Val Pro Xaa Arg Ser Trp
1 5 10

<210> 334
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> MIIP peptide

<220>
<221> X
<222> (7)..(7)
<223> X is K or E

<400> 334

Glu Glu Ser Ala Val Pro Xaa Arg Ser Trp
1 5 10

<210> 335
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> LB-DHX33-1C peptide

<220>
<221> X
<222> (9)..(9)
<223> X is C or R

<400> 335

Tyr Leu Tyr Glu Gly Gly Ile Ser Xaa
1 5

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<223> PANE1 peptide

<400> 336

Arg Val Trp Asp Leu Pro Gly Val Leu Lys
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<210> 337
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<223> SP110 peptide

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<223> X is R or G

<400> 337

Ser Leu Pro Xaa Gly Thr Ser Thr Pro Lys
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<210> 338
<211> 9

<212> PRT
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<220>
<223> ACC-1C/Y

<220>
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<223> X is Y or C

<400> 338

Asp Tyr Leu Gln Xaa Val Leu Gln Ile
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<210> 339
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<223> P2RX7 peptide

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<222> (6)..(6)
<223> X is H or R

<400> 339

Trp Phe His His Cys Xaa Pro Lys Tyr
1 5

<210> 340
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<223> ACC-4 peptide

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<222> (9)..(9)
<223> X is R or G

<400> 340

Ala Thr Leu Pro Leu Leu Cys Ala Xaa
1 5

<210> 341
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<223> ACC-5

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<222> (10)..(10)
<223> X is R or G

<400> 341

Trp Ala Thr Leu Pro Leu Leu Cys Ala Xaa
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<223> X is M or T

<400> 342

Ala Pro Ala Gly Val Arg Glu Val Xaa
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<210> 343
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<220>
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<221> X
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<223> X is K or E

<400> 343

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<220>
<223> APOBEC3H peptide

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<223> X is K or E

<400> 344

Lys Pro Gln Gln Xaa Gly Leu Arg Leu
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<223> LB-ARHGDIB-1R peptide

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<223> X is R or P

<400> 345

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<400> 346

Gln Pro Xaa Arg Ala Leu Leu Phe Val Ile
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<223> X is M or R

<400> 347

Ala Pro Asn Thr Gly Arg Ala Asn Gln Gln Xaa
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<400> 348

Arg Pro Arg Xaa Pro Thr Glu Glu Leu Ala Leu
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Xaa Pro Cys Pro Ser Val Gly Leu Ser Phe Leu
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Asn Pro Ala Thr Pro Xaa Ser Lys Leu
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<223> LB-EBI3-1I peptide

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<223> X is I or V

<400> 351

Arg Pro Arg Ala Arg Tyr Tyr Xaa Gln Val
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<222> (7)..(7)

<223> X is N or K

<400> 352

Leu Pro Gln Lys Lys Ser Xaa Ala Leu
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<222> (7)..(7)

<223> X is L or P

<400> 353

Leu Pro Gln Gln Pro Pro Xaa Ser Leu
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<223> MTRR peptide

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<222> (5)..(5)

<223> X is S or L

<400> 354

Ser Pro Ala Ser Xaa Arg Thr Asp Leu
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<223> LLGL2

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<221> X

<222> (5)..(5)

<223> X is R or H

<400> 355

Ser Pro Ser Leu Xaa Ile Leu Ala Ile
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<212> PRT

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<223> LB-ECGF-1H peptide

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<221> X

<222> (3)..(3)

<223> X is H or R

<400> 356

Arg Pro Xaa Ala Ile Arg Arg Pro Leu Ala Leu
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<223> X is R or P

<400> 357

His Pro Xaa Gln Glu Gln Ile Ala Leu Leu Ala
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<223> X is R or P

<400> 358

His Pro Xaa Gln Glu Gln Ile Ala Leu
1 5

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<400> 359

Arg Leu Arg Gln Xaa Gly Ser Trp Leu
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<210> 360

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<220>

<223> LB-GEMIN4-1V peptide

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<221> X

<222> (9)..(9)

<223> X is V or E

<400> 360

Phe Pro Ala Leu Arg Phe Val Glu Xaa
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<210> 361

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<223> HDGF peptide

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<221> X

<222> (11)..(11)

<223> X is L or P

<400> 361

Leu Pro Met Glu Val Glu Lys Asn Ser Thr Xaa
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<223> LB-PDCD11-1F peptide

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<222> (8)..(8)
<223> X is F or L

<400> 362

Gly Pro Asp Ser Ser Lys Thr Xaa Leu Cys Leu
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<223> X is P or S

<400> 363

Ala Xaa Gly His Thr Arg Arg Lys Leu
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<223> X is S or P

<400> 364

Ala Pro Asp Gly Ala Lys Val Ala Xaa Leu
1 5 10

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<223> X is I or V

<400> 365

Arg Pro Arg Ser Val Thr Xaa Gln Pro Leu Leu
1 5 10

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<223> X is I or T

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Met Pro Ser His Leu Arg Asn Xaa Leu Leu
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<400> 367

Thr Pro Asn Gln Arg Gln Asn Val Cys
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<210> 368
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<221> X
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<223> X is C or S

<400> 368

Xaa Pro Arg Pro Gly Thr Trp Thr Cys
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<210> 369
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<223> X is Y or H

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Arg Pro Arg Xaa Trp Ile Leu Leu Val Lys Ile
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<210> 370
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<223> ZAPHIR peptide

<400> 370

Ile Pro Arg Asp Ser Trp Trp Val Glu Leu
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<210> 371
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<222> (7)..(7)
<223> X is E or G

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Ile Ser Lys Glu Arg Ala Xaa Ala Leu
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<220>
<223> LB-GSTP1-1V peptide

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<221> X
<222> (7)..(7)
<223> X is V or I

<400> 372

Asp Leu Arg Cys Lys Tyr Xaa Ser Leu
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<210> 373
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<223> HA-1/B60 peptide

<220>
<221> X
<222> (6)..(6)
<223> X is H or R

<400> 373

Lys Glu Cys Val Leu Xaa Asp Asp Leu
1 5

<210> 374
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<220>
<223> LB-SON-1R peptide

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<221> X
<222> (6)..(6)
<223> X is R or C

<400> 374

Ser Glu Thr Lys Gln Xaa Thr Val Leu
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<400> 375

Met Glu Gln Leu Glu Xaa Leu Glu Leu
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<400> 376

Gly Xaa Xaa Gln Asp Leu Xaa Thr Leu
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<210> 377
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<223> X is R or Q

<400> 377

Ser Glu Asp Leu Ile Leu Cys Xaa Leu
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<210> 378
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<223> LB-ZNFX1-1Q peptide

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<221> X
<222> (8)..(8)
<223> X is Q or H

<400> 378

Asn Glu Ile Glu Asp Val Trp Xaa Leu Asp Leu
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<223> SLC1A5 peptide

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<222> (3)..(3)

<223> X is A or P

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<223> ACC-2 peptide

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<221> X

<222> (6)..(6)

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Lys Glu Phe Glu Asp Xaa Ile Ile Asn Trp
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<210> 381

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> ACC-6 peptide

<400> 381

Met Glu Ile Phe Ile Glu Val Phe Ser His Phe
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<210> 382

<211> 10

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<220>

<223> HB-1H/Y peptide

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<221> X

<222> (8)..(8)

<223> X is H or Y

<400> 382

Glu Glu Lys Arg Gly Ser Leu Xaa Val Trp
1 5 10

<210> 383

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<221> X

<222> (2)..(2)

<223> X is V or L

<400> 383

Ser Xaa Leu Pro Glu Val Asp Val Trp
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<210> 384

<211> 9

<212> PRT

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<223> UGT2B17/A02 peptide

<400> 384

Cys Val Ala Thr Met Ile Phe Met Ile
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<210> 385

<211> 10

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<223> UGT2B17/A29

<400> 385

Ala Glu Leu Leu Asn Ile Pro Phe Leu Tyr
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<210> 386

<211> 10

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<223> UGT2B17/B44 peptide

<400> 386

Ala Glu Leu Leu Asn Ile Pro Phe Leu Tyr
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<210> 387

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<223> DFFRY peptide

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<222> (4)..(4)

<223> X is C or S

<400> 387

Ile Val Asp Xaa Leu Thr Glu Met Tyr
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<210> 388
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<400> 388

Phe Ile Asp Ser Tyr Ile Cys Gln Val
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<210> 389
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<400> 389

Glu Val Leu Leu Arg Pro Gly Leu His Phe Arg
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<400> 391

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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
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Asp Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asp Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Val Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Val Ser Ile Phe Gly Val Gly Thr 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 Gly Gly Glu Ile Val Met Thr Gln
130 135 140

Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser
145 150 155 160

Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln
165 170 175

Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Asp Ala Ser Asn Arg
180 185 190

Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
195 200 205

Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr
210 215 220

Tyr Cys His Gln Tyr Gly Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr
225 230 235 240

Lys Ala Glu Ile Lys
245

