

SEQUENCE LISTING

<110> Novartis AG

<120> Novel Antibody Molecules and Nucleic Acids

<130> 50886

<160> 70

<170> PatentIn version 3.3

<210> 1

<211> 771

<212> DNA

<213> Artificial

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<223> scFv peptide

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<221> CDS

<222> (1)..(771)

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ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tgc atc atc tct	96
Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser	
20 25 30	
tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa	144
Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu	
35 40 45	
tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg	192
Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro	
50 55 60	
agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc	240
Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr	
65 70 75 80	
gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac	288
Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr	
85 90 95	
tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg	336
Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp	
100 105 110	
ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt	384
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly	
115 120 125	
ggt ggc ggc agc ggc ggc ggc ggc agc gat gtt gtg atg acc cag agc	432
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser	
130 135 140	
ccg agc ttc ctg agc gcg ttc gtt ggt gac cgt atc acc att acc tgc	480
Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys	
145 150 155 160	

cgc gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa gca 528
 Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala
 165 170 175

ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa 576
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln
 180 185 190

acc ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc 624
 Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
 195 200 205

acc ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac 672
 Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 210 215 220

tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa 720
 Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240

gtg gac atc aaa cgc gcg gcc gca ctc gag cac cac cac cac cac cac 768
 Val Asp Ile Lys Arg Ala Ala Ala Leu Glu His His His His His His
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tga 771

<210> 2
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 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

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Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
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Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly

115 120 125

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

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

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

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

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

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

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

Val Asp Ile Lys Arg Ala Ala Ala Leu Glu His His His His His His
245 250 255

<210> 3
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<212> DNA
<213> Artificial

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<220>
<221> CDS
<222> (1)..(774)

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ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tgc atc atc tct 96
Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
20 25 30

tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa 144
Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
35 40 45

tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg 192
Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
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agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc 240

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Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
20 25 30

Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 35 40 45
 Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60
 Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
 65 70 75 80
 Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 85 90 95
 Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser 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 Asp Val Val Met Thr Gln Ser
 130 135 140
 Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys
 145 150 155 160
 Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala
 165 170 175
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln
 180 185 190
 Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
 195 200 205
 Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 210 215 220
 Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240
 Val Asp Ile Lys Arg Ala Ala Ala Leu Glu His His His His His
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 <211> 756
 <212> DNA
 <213> Artificial
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 <223> scFv peptide

<220>

<221> CDS

<222> (1)..(756)

<400> 5

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ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tgc atc atc tct	96
Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser	
20 25 30	
tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa	144
Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu	
35 40 45	
tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg	192
Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro	
50 55 60	
agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc	240
Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr	
65 70 75 80	
gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac	288
Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr	
85 90 95	
tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg	336
Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp	
100 105 110	
ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt	384
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
115 120 125	
ggt ggc ggc agc ggc ggc ggc ggc agc gat gtt gtg atg acc cag agc	432
Gly Gly Gly Ser Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser	
130 135 140	
ccg agc ttc ctg agc gcg ttc gtt ggt gac cgt atc acc att acc tgc	480
Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys	
145 150 155 160	
cgc gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa gca	528
Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala	
165 170 175	
ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa	576
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln	
180 185 190	
acc ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc	624
Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe	
195 200 205	
acc ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac	672
Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr	
210 215 220	
tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa	720
Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys	
225 230 235 240	

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 Val Asp Ile Lys Arg Ala Ala Ala Leu Glu
 245 250

756

<210> 6
 <211> 250
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 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 6

Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
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Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
 100 105 110

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

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

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

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

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

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

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

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

Val Asp Ile Lys Arg Ala Ala Ala Leu Glu
 245 250

<210> 7
 <211> 756
 <212> DNA
 <213> Artificial

<220>
 <223> scFv peptide

<220>
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 <222> (1)..(756)

<220>
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 <222> (85)..(87)
 <223> A codon encoding an amino acid other than cysteine

<400> 7
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 ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt nnn atc atc tct 96
 Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Xaa Ile Ile Ser
 20 25 30
 tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa 144
 Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 35 40 45
 tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg 192
 Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60
 agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc 240
 Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
 65 70 75 80
 gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac 288
 Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 85 90 95
 tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg 336
 Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
 100 105 110
 ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt 384
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly
 115 120 125
 ggt ggc ggc agc ggc ggc ggc ggc agc gat gtt gtg atg acc cag agc 432
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser

130 135 140

ccg agc ttc ctg agc gcg ttc gtt ggt gac cgt atc acc att acc tgc 480
 Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys
 145 150 155 160

cgc gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa gca 528
 Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala
 165 170 175

ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa 576
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln
 180 185 190

acc ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc 624
 Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
 195 200 205

acc ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac 672
 Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 210 215 220

tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa 720
 Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240

gtg gac atc aaa cgc gcg gcc gca ctg gaa taa taa 756
 Val Asp Ile Lys Arg Ala Ala Ala Leu Glu
 245 250

<210> 8
 <211> 250
 <212> PRT
 <213> Artificial

<220>
 <221> misc_feature
 <222> (29)..(29)
 <223> The 'Xaa' at location 29 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, or
 Phe.

<220>
 <223> Synthetic Construct

<400> 8

Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
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Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Xaa Ile Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser 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 Asp Val Val Met Thr Gln Ser
130 135 140

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

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

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

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

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

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

Val Asp Ile Lys Arg Ala Ala Ala Leu Glu
245 250

<210> 9
<211> 774
<212> DNA
<213> Artificial

<220>
<223> scFv peptide

<220>
<221> CDS
<222> (1)..(774)

<220>
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<222> (85)..(87)
<223> A codon encoding an amino acid other than cysteine

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1				5					10				15			
ggt	gaa	tct	ctg	cgt	atc	tct	tgc	aaa	ggt	tct	ggt	nnn	atc	atc	tct	96
Gly	Glu	Ser	Leu	Arg	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Xaa	Ile	Ile	Ser	
			20					25					30			
tct	tac	tgg	atc	agc	tgg	gtt	cgt	cag	atg	ccg	ggc	aag	ggc	ctg	gaa	144
Ser	Tyr	Trp	Ile	Ser	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	
		35					40					45				
tgg	atg	ggt	aaa	att	gat	ccg	ggc	gac	agc	tat	att	aac	tac	agc	ccg	192
Trp	Met	Gly	Lys	Ile	Asp	Pro	Gly	Asp	Ser	Tyr	Ile	Asn	Tyr	Ser	Pro	
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agc	ttt	cag	ggc	cat	gtt	acc	atc	agc	gcc	gat	aaa	agc	att	aac	acc	240
Ser	Phe	Gln	Gly	His	Val	Thr	Ile	Ser	Ala	Asp	Lys	Ser	Ile	Asn	Thr	
65					70					75					80	
gct	tac	ctg	caa	tgg	aac	agc	ctg	aaa	gcg	agc	gac	acc	gcg	atg	tac	288
Ala	Tyr	Leu	Gln	Trp	Asn	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Met	Tyr	
				85					90					95		
tac	tgt	gcc	cgt	ggc	ggg	cgt	gac	ttc	ggt	gat	agc	ttc	gat	tac	tgg	336
Tyr	Cys	Ala	Arg	Gly	Gly	Arg	Asp	Phe	Gly	Asp	Ser	Phe	Asp	Tyr	Trp	
			100					105					110			
ggt	cag	ggc	acc	ctg	gtg	acc	gtg	agc	agc	ggt	ggt	ggc	ggc	agc	ggt	384
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	
		115					120					125				
ggt	ggc	ggc	agc	ggc	ggc	ggc	ggc	agc	gat	gtt	gtg	atg	acc	cag	agc	432
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Val	Val	Met	Thr	Gln	Ser	
		130				135					140					
ccg	agc	ttc	ctg	agc	gcg	ttc	gtt	ggt	gac	cgt	atc	acc	att	acc	tgc	480
Pro	Ser	Phe	Leu	Ser	Ala	Phe	Val	Gly	Asp	Arg	Ile	Thr	Ile	Thr	Cys	
145					150					155					160	
cgc	gcc	agc	agc	ggc	atc	agc	cgc	tat	ctg	gcg	tgg	tat	cag	caa	gca	528
Arg	Ala	Ser	Ser	Gly	Ile	Ser	Arg	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Ala	
				165					170					175		
ccg	ggt	aaa	gca	ccg	aaa	ctg	ctg	atc	tat	gct	gca	agc	acc	ctg	caa	576
Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Thr	Leu	Gln	
			180					185					190			
acc	ggc	gtt	ccg	agc	cgt	ttt	agc	ggt	agc	ggc	agc	ggc	acc	gag	ttc	624
Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Glu	Phe	
		195					200					205				
acc	ctg	acc	atc	aac	agc	ctg	caa	ccg	gag	gat	ttt	gcc	acc	tat	tac	672
Thr</																

<210> 10
 <211> 256
 <212> PRT
 <213> Artificial

<220>
 <221> misc_feature
 <222> (29)..(29)
 <223> The 'Xaa' at location 29 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, or Phe.

<220>
 <223> Synthetic Construct

<400> 10

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Xaa Ile Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser 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 Asp Val Val Met Thr Gln Ser
 130 135 140

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

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

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

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe

195

200

205

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

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

Val Asp Ile Lys Arg Ala Ala Ala Leu Glu His His His His His His
 245 250 255

<210> 11
 <211> 744
 <212> DNA
 <213> Artificial

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<220>
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<400> 11
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 ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tgc atc atc tct 96
 Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
 20 25 30
 tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa 144
 Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 35 40 45
 tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg 192
 Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60
 agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc 240
 Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
 65 70 75 80
 gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac 288
 Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 85 90 95
 tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg 336
 Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
 100 105 110
 ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt 384
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125
 ggt ggc ggc agc ggc ggc ggc ggc agc gat gtt gtg atg acc cag agc 432
 Gly Gly Gly Ser Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser
 130 135 140
 ccg agc ttc ctg agc gcg ttc gtt ggt gac cgt atc acc att acc tgc 480

65

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

cgc gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa gca 528
 Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala
 165 170 175

ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa 576
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln
 180 185 190

acc ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc 624
 Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
 195 200 205

acc ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac 672
 Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 210 215 220

tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa 720
 Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240

gtg gac atc aaa cgc gcg taa taa 744
 Val Asp Ile Lys Arg Ala
 245

<210> 12
 <211> 246
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 12

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
 100 105 110

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

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

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

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

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

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

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

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

Val Asp Ile Lys Arg Ala
 245

<210> 13
 <211> 744
 <212> DNA
 <213> Artificial

<220>
 <223> scFv peptide

<220>
 <221> CDS
 <222> (1)..(744)
 <220>
 <221> misc_feature
 <222> (85)..(87)
 <223> A codon encoding an amino acid other than cysteine

<400> 13
 atg gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg 48
 Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
 1 5 10 15

ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt nnn atc atc tct 96
 Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Xaa Ile Ile Ser
 20 25 30

tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa 144
 Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 35 40 45

tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg 192
 Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60
 agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc 240
 Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
 65 70 75 80
 gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac 288
 Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 85 90 95
 tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg 336
 Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
 100 105 110
 ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt 384
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125
 ggt ggc ggc agc ggc ggc ggc ggc agc gat gtt gtg atg acc cag agc 432
 Gly Gly Gly Ser Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser
 130 135 140
 ccg agc ttc ctg agc gcg ttc gtt ggt gac cgt atc acc att acc tgc 480
 Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys
 145 150 155 160
 cgc gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa gca 528
 Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala
 165 170 175
 ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa 576
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln
 180 185 190
 acc ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc 624
 Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
 195 200 205
 acc ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac 672
 Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 210 215 220
 tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa 720
 Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240
 gtg gac atc aaa cgc gcg taa taa 744
 Val Asp Ile Lys Arg Ala
 245

<210> 14

<211> 246

<212> PRT

<213> Artificial

<220>

<221> misc_feature

<222> (29)..(29)

<223> The 'Xaa' at location 29 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, or Phe.

<220>

<223> Synthetic Construct

<400> 14

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Xaa Ile Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser 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 Asp Val Val Met Thr Gln Ser
 130 135 140

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

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

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

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

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

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

Val Asp Ile Lys Arg Ala

245

<210> 15
 <211> 744
 <212> DNA
 <213> Artificial

<220>
 <223> scFv peptide

<220>
 <221> CDS
 <222> (1)..(744).

<400> 15
 atg gcg gaa gtg cag ctg gtt gaa tct ggt gct gaa gtt aaa aaa ccg 48
 Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
 1 5 10 15

ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tgc atc atc tct 96
 Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
 20 25 30

tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa 144
 Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 35 40 45

tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg 192
 Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc 240
 Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
 65 70 75 80

gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac 288
 Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 85 90 95

tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg 336
 Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
 100 105 110

ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt 384
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125

ggt ggc ggc agc ggc ggc ggc ggc agc gat gtt gtg atg acc cag agc 432
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser
 130 135 140

ccg agc ttc ctg agc gcg ttc gtt ggt gac cgt atc acc att acc tgc 480
 Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys
 145 150 155 160

cgc gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa gca 528
 Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala
 165 170 175

ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa 576
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln
 180 185 190

acc ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc 624

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

acc ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac 672
 Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 210 215 220

tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa 720
 Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240

gtg gac atc aaa cgc gcg taa taa 744
 Val Asp Ile Lys Arg Ala
 245

<210> 16
 <211> 246
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 16

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
 100 105 110

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

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

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

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

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

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

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

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

Val Asp Ile Lys Arg Ala
 245

<210> 17
 <211> 744
 <212> DNA
 <213> Artificial

<220>
 <223> scFv peptide

<220>
 <221> CDS
 <222> (1)..(744)
 <220>
 <221> misc_feature
 <222> (85)..(87)
 <223> A codon encoding an amino acid other than cysteine

<400> 17
 atg gcg gaa gtg cag ctg gtt gaa tct ggt gct gaa gtt aaa aaa ccg 48
 Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
 1 5 10 15
 ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt nnn atc atc tct 96
 Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Xaa Ile Ile Ser
 20 25 30
 tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa 144
 Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 35 40 45
 tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg 192
 Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60
 agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc 240
 Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
 65 70 75 80
 gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac 288
 Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 85 90 95

tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg 336
 Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
 100 105 110
 ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt 384
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125
 ggt ggc ggc agc ggc ggc ggc ggc agc gat gtt gtg atg acc cag agc 432
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser
 130 135 140
 ccg agc ttc ctg agc gcg ttc gtt ggt gac cgt atc acc att acc tgc 480
 Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys
 145 150 155 160
 cgc gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa gca 528
 Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala
 165 170 175
 ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa 576
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln
 180 185 190
 acc ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc 624
 Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
 195 200 205
 acc ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac 672
 Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 210 215 220
 tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa 720
 Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240
 gtg gac atc aaa cgc gcg taa taa 744
 Val Asp Ile Lys Arg Ala
 245

<210> 18
 <211> 246
 <212> PRT
 <213> Artificial

<220>
 <221> misc_feature
 <222> (29)..(29)
 <223> The 'Xaa' at location 29 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, or
 Phe.

<220>
 <223> Synthetic Construct

<400> 18

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Xaa Ile Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser 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 Asp Val Val Met Thr Gln Ser
 130 135 140

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

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

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

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

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

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

Val Asp Ile Lys Arg Ala
 245

<210> 19

<211> 774

<212> DNA

<213> Artificial

<220>

<223> scFv peptide

<220>

<221> CDS

<222> (1)..(774)

<400> 19

atg gcg gaa gtg cag ctg gtt gaa tct ggt gct gaa gtt aaa aaa ccg	48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro	
1 5 10 15	
ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tgc atc atc tct	96
Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser	
20 25 30	
tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa	144
Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu	
35 40 45	
tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg	192
Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro	
50 55 60	
agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc	240
Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr	
65 70 75 80	
gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac	288
Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr	
85 90 95	
tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg	336
Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp	
100 105 110	
ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt	384
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
115 120 125	
ggt ggc ggc agc ggc ggc ggc ggc agc gat gtt gtg atg acc cag agc	432
Gly Gly Gly Ser Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser	
130 135 140	
ccg agc ttc ctg agc gcg ttc gtt ggt gac cgt atc acc att acc tgc	480
Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys	
145 150 155 160	
cgc gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa gca	528
Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala	
165 170 175	
ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa	576
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln	
180 185 190	
acc ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc	624
Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe	
195 200 205	
acc ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac	672
Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr	
210 215 220	
tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa	720
Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys	
225 230 235 240	
gtg gac atc aaa cgc gcg gcc gca ctc gag cac cac cac cac cac	768

Val Asp Ile Lys Arg Ala Ala Ala Leu Glu His His His His His His
 245 250 255

taa taa

774

<210> 20
 <211> 256
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 20

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser 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 Asp Val Val Met Thr Gln Ser
 130 135 140

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

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

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

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

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

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

Val Asp Ile Lys Arg Ala Ala Ala Leu Glu His His His His His His
245 250 255

<210> 21

<211> 774

<212> DNA

<213> Artificial

<220>

<223> scFv peptide

<220>

<221> CDS

<222> (1)..(774)

<220>

<221> misc_feature

<222> (85)..(87)

<223> A codon encoding an amino acid other than cysteine

<400> 21

atg gcg gaa gtg cag ctg gtt gaa tct ggt gct gaa gtt aaa aaa ccg 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
1 5 10 15

ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt nnn atc atc tct 96
Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Xaa Ile Ile Ser
20 25 30

tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa 144
Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
35 40 45

tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg 192
Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
50 55 60

agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc 240
Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac 288
Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
85 90 95

tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg 336
Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
100 105 110

ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt 384
Gly Gln Gly Thr Leu Val Thr Ser Ser Gly Gly Gly Ser Gly
115 120 125

ggt ggc ggc agc ggc ggc ggc ggc agc gat gtt gtg atg acc cag agc 432

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

ccg agc ttc ctg agc gcg ttc gtt ggt gac cgt atc acc att acc tgc 480
 Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys
 145 150 155 160

cgc gcc agc agc gcc atc agc cgc tat ctg gcg tgg tat cag caa gca 528
 Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala
 165 170 175

ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa 576
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln
 180 185 190

acc gcc gtt ccg agc cgt ttt agc ggt agc gcc agc gcc acc gag ttc 624
 Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
 195 200 205

acc ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac 672
 Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 210 215 220

tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt gcc gcc acc aaa 720
 Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240

gtg gac atc aaa cgc gcg gcc gca ctc gag cac cac cac cac cac 768
 Val Asp Ile Lys Arg Ala Ala Ala Leu Glu His His His His His His
 245 250 255

taa taa 774

<210> 22
 <211> 256
 <212> PRT
 <213> Artificial

<220>
 <221> misc feature
 <222> (29)..(29)
 <223> The 'Xaa' at location 29 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, or
 Phe.

<220>
 <223> Synthetic Construct

<400> 22

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Xaa Ile Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser 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 Asp Val Val Met Thr Gln Ser
130 135 140

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

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

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

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

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

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

Val Asp Ile Lys Arg Ala Ala Ala Leu Glu His His His His His His
245 250 255

<210> 23

<211> 744

<212> DNA

<213> Artificial

<220>

<223> scFv peptide

<220>

<221> CDS

<222> (1)..(744)

<400> 23

atg gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg
Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
1 5 10 15

ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tat agc atc tct Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser 20 25 30	96
tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu 35 40 45	144
tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro 50 55 60	192
agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr 65 70 75 80	240
gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr 85 90 95	288
tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp 100 105 110	336
ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly 115 120 125	384
ggt ggc ggc agc ggc ggc ggc ggc agc gat gtt gtg atg acc cag agc Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser 130 135 140	432
ccg agc tcc ctg agc gcg agc gtt ggt gac cgt atc acc att acc tgc Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Ile Thr Ile Thr Cys 145 150 155 160	480
cgc gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa gca Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala 165 170 175	528
ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln 180 185 190	576
acc ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe 195 200 205	624
acc ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr 210 215 220	672
tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys 225 230 235 240	720
gtg gac atc aaa cgc gcg taa taa Val Asp Ile Lys Arg Ala 245	744

<210> 24
 <211> 246
 <212> PRT
 <213> Artificial

<220>

<223> Synthetic Construct

<400> 24

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser 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 Asp Val Val Met Thr Gln Ser
 130 135 140

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

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

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

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

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

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

Val Asp Ile Lys Arg Ala
245

<210> 25

<211> 744

<212> DNA

<213> Artificial

<220>

<223> scFv peptide

<220>

<221> CDS

<222> (1)..(744)

<400> 25

atg gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
1 5 10 15

ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tat agc atc tct 96
Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser
20 25 30

tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa 144
Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
35 40 45

tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg 192
Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
50 55 60

agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc 240
Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac 288
Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
85 90 95

tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg 336
Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
100 105 110

ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt 384
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

ggt ggc ggc agc ggc ggc ggc ggc agc gat att cag atg acc cag agc 432
Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
130 135 140

ccg agc tcc ctg agc gcg agc gtt ggt gac cgt atc acc att acc tgc 480
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Ile Thr Ile Thr Cys
145 150 155 160

cgc gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa gca 528
Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala
165 170 175

ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa 576
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln
180 185 190

acc ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc 624
 Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
 195 200 205

acc ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac 672
 Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 210 215 220

tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa 720
 Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240

gtg gac atc aaa cgc gcg taa taa 744
 Val Asp Ile Lys Arg Ala
 245

<210> 26
 <211> 246
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 26

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

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

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

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

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

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

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

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

Val Asp Ile Lys Arg Ala
 245

<210> 27
 <211> 744
 <212> DNA
 <213> Artificial

<220>
 <223> scFv peptide

<220>
 <221> CDS
 <222> (1)..(744)

<400> 27
 atg gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg 48
 Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
 1 5 10 15
 ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tgc atc atc tct 96
 Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
 20 25 30
 tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa 144
 Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 35 40 45
 tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg 192
 Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60
 agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc 240
 Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
 65 70 75 80
 gct tac ctg caa tgg agc agc ctg aaa gcg agc gac acc gcg atg tac 288
 Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 85 90 95
 tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg 336
 Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
 100 105 110

ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt 384
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125
 ggt ggc ggc agc ggc ggc ggc ggc agc gat att cag atg acc cag agc 432
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 130 135 140
 ccg agc ttc ctg agc ggc ttc gtt ggt gac cgt atc acc att acc tgc 480
 Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys
 145 150 155 160
 cgc gcc agc agc ggc atc agc cgc tat ctg ggc tgg tat cag caa aaa 528
 Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Lys
 165 170 175
 ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa 576
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln
 180 185 190
 acc ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc 624
 Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
 195 200 205
 acc ctg acc atc agc agc ctg caa ccg gag gat ttt gcc acc tat tac 672
 Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 210 215 220
 tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa 720
 Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240
 gtg gac atc aaa cgc ggc taa taa 744
 Val Asp Ile Lys Arg Ala
 245

<210> 28
 <211> 246
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 28

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
85 90 95

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

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

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

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

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu 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 His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Asp Ile Lys Arg Ala
245

<210> 29
<211> 759
<212> DNA
<213> Artificial

<220>
<223> scFv peptide

<220>
<221> CDS
<222> (1)..(759)

<400> 29
atg gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
1 5 10 15
ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tgc atc atc tct 96
Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser

20	25	30	
tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa			144
Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu			
35	40	45	
tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg			192
Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro			
50	55	60	
agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc			240
Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr			
65	70	75	80
gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac			288
Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr			
85	90	95	
tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg			336
Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp			
100	105	110	
ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt			384
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly			
115	120	125	
ggt ggc gga tcc ggt ggt ggc ggc agc ggc ggc ggc ggc agc gat gtt			432
Gly Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Val			
130	135	140	
gtg atg acc cag agc ccg agc ttc ctg agc gcg ttc gtt ggt gac cgt			480
Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg			
145	150	155	160
atc acc att acc tgc cgc gcc agc agc ggc atc agc cgc tat ctg gcg			528
Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala			
165	170	175	
tgg tat cag caa gca ccg ggt aaa gca ccg aaa ctg ctg atc tat gct			576
Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala			
180	185	190	
gca agc acc ctg caa acc ggc gtt ccg agc cgt ttt agc ggt agc ggc			624
Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly			
195	200	205	
agc ggc acc gag ttc acc ctg acc atc aac agc ctg caa ccg gag gat			672
Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp			
210	215	220	
ttt gcc acc tat tac tgc caa cac ctg aat agc tat ccg ctg acc ttc			720
Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe			
225	230	235	240
ggt ggc ggc acc aaa gtg gac atc aaa cgc gcg taa taa			759
Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala			
245	250		

<210> 30
 <211> 251
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 30

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
 100 105 110

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

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val
 130 135 140

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

Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala
 165 170 175

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

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

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

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

Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala
 245 250

<210> 31
 <211> 762
 <212> DNA
 <213> Artificial

<220>
 <223> scFv peptide

<220>
 <221> CDS
 <222> (1)..(762)

<400> 31
 atg gat gtt gtg atg acc cag agc ccg agc ttc ctg agc gcg ttc gtt 48
 Met Asp Val Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Phe Val
 1 5 10 15
 ggt gac cgt atc acc att acc tgc cgc gcc agc agc ggc atc agc cgc 96
 Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg
 20 25 30
 tat ctg gcg tgg tat cag caa gca ccg ggt aaa gca ccg aaa ctg ctg 144
 Tyr Leu Ala Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys Leu Leu
 35 40 45
 atc tat gct gca agc acc ctg caa acc ggc gtt ccg agc cgt ttt agc 192
 Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser
 50 55 60
 ggt agc ggc agc ggc acc gag ttc acc ctg acc atc aac agc ctg caa 240
 Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Gln
 65 70 75 80
 ccg gag gat ttt gcc acc tat tac tgc caa cac ctg aat agc tat ccg 288
 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Pro
 85 90 95
 ctg acc ttc ggt ggc ggc acc aaa gtg gac atc aaa cgc gcg agc ggt 336
 Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ser Gly
 100 105 110
 ggt ggc ggc agc ggt ggt ggc gga tcc ggt ggt ggc ggc agc ggc ggc 384
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 115 120 125
 ggc ggc agc gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa 432
 Gly Gly Ser Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys
 130 135 140
 aaa ccg ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tgc atc 480
 Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile
 145 150 155 160
 atc tct tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc 528
 Ile Ser Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly
 165 170 175
 ctg gaa tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac 576
 Leu Glu Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr
 180 185 190
 agc ccg agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att 624
 Ser Pro Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile
 195 200 205

aac acc gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg 672
 Asn Thr Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala
 210 215 220

atg tac tac tgt gcc cgt gcc ggt cgt gac ttc ggt gat agc ttc gat 720
 Met Tyr Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp
 225 230 235 240

tac tgg ggt cag gcc acc ctg gtg acc gtg agc agc taa taa 762
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 245 250

<210> 32
 <211> 252
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 32

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

Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg
 20 25 30

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

Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser
 50 55 60

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

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

Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ser Gly
 100 105 110

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

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

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

Ile Ser Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly
 165 170 175

Leu Glu Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr
 180 185 190

Ser Pro Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile
 195 200 205

Asn Thr Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala
 210 215 220

Met Tyr Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp
 225 230 235 240

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 245 250

<210> 33

<211> 774

<212> DNA

<213> Artificial

<220>

<223> scFv peptide

<220>

<221> CDS

<222> (1)..(774)

<220>

<221> misc_feature

<222> (292)..(294)

<223> n is a, c, g, or t

<400> 33

atg gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg 48
 Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
 1 5 10 15

ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tgc atc atc tct 96
 Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
 20 25 30

tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa 144
 Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 35 40 45

tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg 192
 Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc 240
 Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
 65 70 75 80

gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac 288
 Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 85 90 95

tac nnn gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg 336

Tyr Xaa Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
 100 105 110
 ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt 384
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125
 ggt ggc ggc agc ggc ggc ggc ggc agc gat gtt gtg atg acc cag agc 432
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser
 130 135 140
 ccg agc ttc ctg agc gcg ttc gtt ggt gac cgt atc acc att acc tgc 480
 Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys
 145 150 155 160
 cgc gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa gca 528
 Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala
 165 170 175
 ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa 576
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln
 180 185 190
 acc ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc 624
 Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
 195 200 205
 acc ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac 672
 Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 210 215 220
 tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa 720
 Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240
 gtg gac atc aaa cgc gcg gcc gca ctc gag cac cac cac cac cac cac 768
 Val Asp Ile Lys Arg Ala Ala Ala Leu Glu His His His His His His
 245 250 255
 taa taa 774

<210> 34
 <211> 256
 <212> PRT
 <213> Artificial

<220>
 <221> misc_feature
 <222> (98)..(98)
 <223> The 'Xaa' at location 98 stands for Lys, Asn, Arg, Ser, Thr, Ile,
 Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, Tyr, Trp, or
 Phe.

<220>
 <223> Synthetic Construct

<400> 34

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
50 55 60

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

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

Tyr Xaa Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser 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 Asp Val Val Met Thr Gln Ser
130 135 140

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

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

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

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

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

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

Val Asp Ile Lys Arg Ala Ala Ala Leu Glu His His His His His His
245 250 255

<210> 35

<211> 744

<212> DNA

<213> Artificial

<220>

<223> scFv peptide

<220>

<221> CDS

<222> (1)..(744)

<400> 35

atg gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg	48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro	
1 5 10 15	
ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tat agc atc tct	96
Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser	
20 25 30	
tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa	144
Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu	
35 40 45	
tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg	192
Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro	
50 55 60	
agc ttt cag ggc cgt gtt acc atc agc gcc gat aaa agc att aac acc	240
Ser Phe Gln Gly Arg Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr	
65 70 75 80	
gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac	288
Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr	
85 90 95	
tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg	336
Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp	
100 105 110	
ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt	384
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly	
115 120 125	
ggt ggc ggc agc ggc ggc ggc ggc agc gat att cag atg acc cag agc	432
Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser	
130 135 140	
ccg agc tcc ctg agc gcg agc gtt ggt gac cgt atc acc att acc tgc	480
Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Ile Thr Ile Thr Cys	
145 150 155 160	
cgc gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa gca	528
Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala	
165 170 175	
ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa	576
Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln	
180 185 190	
acc ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc	624
Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe	
195 200 205	
acc ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac	672
Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr	
210 215 220	
tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa	720
Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys	
225 230 235 240	
gtg gac atc aaa cgc gcg taa taa	744

Val Asp Ile Lys Arg Ala
245

<210> 36
<211> 246
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 36

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser
20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
50 55 60

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

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

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

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

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

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

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

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

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

Val Asp Ile Lys Arg Ala
 245

<210> 37
 <211> 744
 <212> DNA
 <213> Artificial

<220>
 <223> scFv peptide

<220>
 <221> CDS
 <222> (1)..(744)

<400> 37
 atg gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg 48
 Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
 1 5 10 15
 ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tat agc atc tct 96
 Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser
 20 25 30
 tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa 144
 Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
 35 40 45
 tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg 192
 Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60
 agc ttt cag ggc cgt gtt acc atc agc gcc gat aaa agc att aac acc 240
 Ser Phe Gln Gly Arg Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
 65 70 75 80
 gct tac ctg caa tgg agc agc ctg aaa gcg agc gac acc gcg atg tac 288
 Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 85 90 95
 tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg 336
 Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
 100 105 110
 ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt 384
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly
 115 120 125
 ggt ggc ggc agc ggc ggc ggc ggc agc gat att cag atg acc cag agc 432
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
 130 135 140
 ccg agc tcc ctg agc gcg agc gtt ggt gac cgt atc acc att acc tgc 480
 Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Ile Thr Ile Thr Cys
 145 150 155 160

cgc gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa aaa 528
 Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Lys
 165 170 175

ccg ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa 576
 Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln
 180 185 190

acc ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc 624
 Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
 195 200 205

acc ctg acc atc agc agc ctg caa ccg gag gat ttt gcc acc tat tac 672
 Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
 210 215 220

tgc caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa 720
 Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
 225 230 235 240

gtg gac atc aaa cgc gcg taa taa 744
 Val Asp Ile Lys Arg Ala
 245

<210> 38
 <211> 246
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 38

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

Ala Tyr Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 85 90 95

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

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

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

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

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu 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 His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys
225 230 235 240

Val Asp Ile Lys Arg Ala
245

<210> 39
<211> 774
<212> DNA
<213> Artificial

<220>
<223> scFv peptide

<220>
<221> CDS
<222> (1)..(774)

<400> 39
atg gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
1 5 10 15
ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tgc atc atc tct 96
Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
20 25 30
tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa 144
Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
35 40 45
tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg 192
Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
50 55 60
agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc 240
Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac 288
 Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
 85 90 95

tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg 336
 Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
 100 105 110

ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt 384
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125

ggt ggc gga tcc ggt ggt ggc ggc tcc ggt ggt ggc ggc agc ggc ggc 432
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 130 135 140

ggc ggc agc gat gtt gtg atg acc cag agc ccg agc ttc ctg agc gcg 480
 Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala
 145 150 155 160

ttc gtt ggt gac cgt atc acc att acc tgc cgc gcc agc agc ggc atc 528
 Phe Val Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile
 165 170 175

agc cgc tat ctg gcg tgg tat cag caa gca ccg ggt aaa gca ccg aaa 576
 Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys
 180 185 190

ctg ctg atc tat gct gca agc acc ctg caa acc ggc gtt ccg agc cgt 624
 Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg
 195 200 205

ttt agc ggt agc ggc agc ggc acc gag ttc acc ctg acc atc aac agc 672
 Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser
 210 215 220

ctg caa ccg gag gat ttt gcc acc tat tac tgc caa cac ctg aat agc 720
 Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser
 225 230 235 240

tat ccg ctg acc ttc ggt ggc ggc acc aaa gtg gac atc aaa cgc gcg 768
 Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala
 245 250 255

taa taa 774

<210> 40
 <211> 256
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 40

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser 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 Gly Gly Ser Gly Gly
130 135 140

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

Phe Val Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile
165 170 175

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

Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg
195 200 205

Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser
210 215 220

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

Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala
245 250 255

<210> 41

<211> 789

<212> DNA

<213> Artificial

<220>

<223> scFv peptide

<220>

<221> CDS

<222> (1)..(789)

<400> 41

atg gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg	48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro	
1 5 10 15	
ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tgc atc atc tct	96
Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser	
20 25 30	
tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa	144
Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu	
35 40 45	
tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg	192
Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro	
50 55 60	
agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc	240
Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr	
65 70 75 80	
gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac	288
Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr	
85 90 95	
tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg	336
Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp	
100 105 110	
ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt	384
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly	
115 120 125	
ggt ggc gga tct ggt ggt ggc ggc agc ggt ggt ggc gga tcc ggt ggt	432
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
130 135 140	
ggc ggc agc ggc ggc ggc ggc agc gat gtt gtg atg acc cag agc ccg	480
Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro	
145 150 155 160	
agc ttc ctg agc gcg ttc gtt ggt gac cgt atc acc att acc tgc cgc	528
Ser Phe Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys Arg	
165 170 175	
gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa gca ccg	576
Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala Pro	
180 185 190	
ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa acc	624
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Thr	
195 200 205	
ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc acc	672
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr	
210 215 220	
ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac tgc	720
Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys	
225 230 235 240	
caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa gtg	768
Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val	

245

250

255

gac atc aaa cgc gcg taa taa
 Asp Ile Lys Arg Ala
 260

789

<210> 42
 <211> 261
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 42

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser 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 Gly Gly Ser Gly Gly
 130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro
 145 150 155 160

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

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

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Thr

195

200

205

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 210 215 220

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

Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 245 250 255

Asp Ile Lys Arg Ala
 260

<210> 43

<211> 777

<212> DNA

<213> Artificial

<220>

<223> scFv peptide

<220>

<221> CDS

<222> (1)..(777)

<400> 43

atg gat gtt gtg atg acc cag agc ccg agc ttc ctg agc gcg ttc gtt 48
 Met Asp Val Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Phe Val
 1 5 10 15

ggt gac cgt atc acc att acc tgc cgc gcc agc agc ggc atc agc cgc 96
 Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg
 20 25 30

tat ctg gcg tgg tat cag caa gca ccg ggt aaa gca ccg aaa ctg ctg 144
 Tyr Leu Ala Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys Leu Leu
 35 40 45

atc tat gct gca agc acc ctg caa acc ggc gtt ccg agc cgt ttt agc 192
 Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser
 50 55 60

ggt agc ggc agc ggc acc gag ttc acc ctg acc atc aac agc ctg caa 240
 Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Gln
 65 70 75 80

ccg gag gat ttt gcc acc tat tac tgc caa cac ctg aat agc tat ccg 288
 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Pro
 85 90 95

ctg acc ttc ggt ggc ggc acc aaa gtg gac atc aaa cgc gcg agc ggt 336
 Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ser Gly
 100 105 110

ggt ggc ggc agc ggt ggt ggc gga tcc ggt ggt ggc ggc tcc ggt ggt 384
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
 115 120 125

ggc ggc agc ggc ggc ggc ggc agc gct gaa gtt caa ctt gtt gaa tct 432

Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Val Gln Leu Val Glu Ser
 130 135 140

ggt gct gaa gtt aaa aaa ccg ggt gaa tct ctg cgt atc tct tgc aaa 480
 Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys
 145 150 155 160

ggt tct ggt tgc atc atc tct tct tac tgg atc agc tgg gtt cgt cag 528
 Gly Ser Gly Cys Ile Ile Ser Ser Tyr Trp Ile Ser Trp Val Arg Gln
 165 170 175

atg ccg ggc aag ggc ctg gaa tgg atg ggt aaa att gat ccg ggc gac 576
 Met Pro Gly Lys Gly Leu Glu Trp Met Gly Lys Ile Asp Pro Gly Asp
 180 185 190

agc tat att aac tac agc ccg agc ttt cag ggc cat gtt acc atc agc 624
 Ser Tyr Ile Asn Tyr Ser Pro Ser Phe Gln Gly His Val Thr Ile Ser
 195 200 205

gcc gat aaa agc att aac acc gct tac ctg caa tgg aac agc ctg aaa 672
 Ala Asp Lys Ser Ile Asn Thr Ala Tyr Leu Gln Trp Asn Ser Leu Lys
 210 215 220

gcg agc gac acc gcg atg tac tac tgt gcc cgt ggc ggt cgt gac ttc 720
 Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Gly Gly Arg Asp Phe
 225 230 235 240

ggt gat agc ttc gat tac tgg ggt cag ggc acc ctg gtg acc gtg agc 768
 Gly Asp Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 245 250 255

agc taa taa 777
 Ser

<210> 44
 <211> 257
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 44

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

Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg
 20 25 30

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

Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser
 50 55 60

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

104

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

Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ser Gly
100 105 110

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

Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Val Gln Leu Val Glu Ser
130 135 140

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

Gly Ser Gly Cys Ile Ile Ser Ser Tyr Trp Ile Ser Trp Val Arg Gln
165 170 175

Met Pro Gly Lys Gly Leu Glu Trp Met Gly Lys Ile Asp Pro Gly Asp
180 185 190

Ser Tyr Ile Asn Tyr Ser Pro Ser Phe Gln Gly His Val Thr Ile Ser
195 200 205

Ala Asp Lys Ser Ile Asn Thr Ala Tyr Leu Gln Trp Asn Ser Leu Lys
210 215 220

Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Gly Gly Arg Asp Phe
225 230 235 240

Gly Asp Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
245 250 255

Ser

<210> 45

<211> 792

<212> DNA

<213> Artificial

<220>

<223> scFv peptide

<220>

<221> CDS

<222> (1)..(792)

<400> 45

atg gat gtt gtg atg acc cag agc ccg agc ttc ctg agc gcg ttc gtt
Met Asp Val Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Phe Val
1 5 10 15 48

ggt gac cgt atc acc att acc tgc cgc gcc agc agc ggc atc agc cgc Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg 20 25 30	96
tat ctg gcg tgg tat cag caa gca ccg ggt aaa gca ccg aaa ctg ctg Tyr Leu Ala Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys Leu Leu 35 40 45	144
atc tat gct gca agc acc ctg caa acc ggc gtt ccg agc cgt ttt agc Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser 50 55 60	192
ggt agc ggc agc ggc acc gag ttc acc ctg acc atc aac agc ctg caa Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Gln 65 70 75 80	240
ccg gag gat ttt gcc acc tat tac tgc caa cac ctg aat agc tat ccg Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Pro 85 90 95	288
ctg acc ttc ggt ggc ggc acc aaa gtg gac atc aaa cgc gcg agc ggt Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ser Gly 100 105 110	336
ggt ggc ggc agc ggt ggt ggc gga tct ggt ggt ggc ggc agc ggt ggt Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly 115 120 125	384
ggc gga tcc ggt ggt ggc ggc agc ggc ggc ggc ggc agc gct gaa gtt Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ala Glu Val 130 135 140	432
caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg ggt gaa tct ctg Gln Leu Val Glu Ser Lys Ala Glu Val Lys Lys Pro Gly Glu Ser Leu 145 150 155 160	480
cgt atc tct tgc aaa ggt tct ggt tgc atc atc tct tct tac tgg atc Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser Ser Tyr Trp Ile 165 170 175	528
agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa tgg atg ggt aaa Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Lys 180 185 190	576
att gat ccg ggc gac agc tat att aac tac agc ccg agc ttt cag ggc Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro Ser Phe Gln Gly 195 200 205	624
cat gtt acc atc agc gcc gat aaa agc att aac acc gct tac ctg caa His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr Leu Gln 210 215 220	672
tgg aac agc ctg aaa gcg agc gac acc gcg atg tac tac tgt gcc cgt Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg 225 230 235 240	720
ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg ggt cag ggc acc Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp Gly Gln Gly Thr 245 250 255	768
ctg gtg acc gtg agc agc taa taa Leu Val Thr Val Ser Ser 260	792

<211> 262
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 46

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

Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg
 20 25 30

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

Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser
 50 55 60

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

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

Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ser Gly
 100 105 110

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Val
 130 135 140

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

Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser Ser Tyr Trp Ile
 165 170 175

Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Lys
 180 185 190

Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro Ser Phe Gln Gly
 195 200 205

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

Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg

Leu Val Thr Val Ser Ser
260

<210>	47
<211>	759
<212>	DNA
<213>	Artificial

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<220>
<223>  scFv peptide
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<220>
<221> CDS
<222> (1) .. (759)
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<400>	47																	
atg gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg																		48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro																		
1				5				10					15					
ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tat agc atc tct																		96
Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser																		
			20				25						30					
tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa																		144
Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu																		
			35				40					45						
tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg																		192
Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro																		
			50			55					60							
agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc																		240
Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr																		
65					70			75								80		
gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac																		288
Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr																		
				85				90							95			
tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg																		336
Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp																		
			100				105						110					
ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt																		384
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly																		
			115				120					125						
ggt ggc gga tcc ggt ggt ggc ggc agc ggc ggc ggc ggc agc gat gtt																		432
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val																		
			130			135						140						
gtg atg acc cag agc ccg agc ttc ctg agc gcg ttc gtt ggt gac cgt																		480
Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg																		
145					150				155							160		
atc acc att acc tgc cgc gcc agc agc gcc atc agc cgc tat ctg gcg																		528

108

Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala
 165 170 175
 tgg tat cag caa gca ccg ggt aaa gca ccg aaa ctg ctg atc tat gct 576
 Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 180 185 190
 gca agc acc ctg caa acc ggc gtt ccg agc cgt ttt agc ggt agc ggc 624
 Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 195 200 205
 agc ggc acc gag ttc acc ctg acc atc aac agc ctg caa ccg gag gat 672
 Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp
 210 215 220
 ttt gcc acc tat tac tgc caa cac ctg aat agc tat ccg ctg acc ttc 720
 Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe
 225 230 235 240
 ggt ggc ggc acc aaa gtg gac atc aaa cgc gcg taa taa 759
 Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala
 245 250

 <210> 48
 <211> 251
 <212> PRT
 <213> Artificial

 <220>
 <223> Synthetic Construct

 <400> 48

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

 Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser
 20 25 30

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

 Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

 Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser 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 Gly Gly Ser Asp Val
130 135 140

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

Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala
165 170 175

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

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

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

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

Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala
245 250

<210> 49
<211> 774
<212> DNA
<213> Artificial

<220>
<223> scFv peptide

<220>
<221> CDS
<222> (1)..(774)

<400> 49
atg gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg 48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro
1 5 10 15
ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tat agc atc tct 96
Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser
20 25 30
tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa 144
Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu
35 40 45
tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg 192
Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
50 55 60
agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc 240
Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr
65 70 75 80

110

gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac 288
Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr
85 90 95

tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg 336
Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp
100 105 110

ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt 384
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Ser Gly
115 120 125

ggt ggc gga tcc ggt ggt ggc ggc tcc ggt ggt ggc ggc agc ggc ggc 432
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
130 135 140

ggc ggc agc gat gtt gtg atg acc cag agc ccg agc ttc ctg agc gcg 480
Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala
145 150 155 160

ttc gtt ggt gac cgt atc acc att acc tgc cgc gcc agc agc ggc atc 528
Phe Val Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile
165 170 175

agc cgc tat ctg gcg tgg tat cag caa gca ccg ggt aaa gca ccg aaa 576
Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys
180 185 190

ctg ctg atc tat gct gca agc acc ctg caa acc ggc gtt ccg agc cgt 624
Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg
195 200 205

ttt agc ggt agc ggc agc ggc acc gag ttc acc ctg acc atc aac agc 672
Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser
210 215 220

ctg caa ccg gag gat ttt gcc acc tat tac tgc caa cac ctg aat agc 720
Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser
225 230 235 240

tat ccg ctg acc ttc ggt ggc ggc acc aaa gtg gac atc aaa cgc gcg 768
Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala
245 250 255

taa taa 774

<210> 50
<211> 256
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 50

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser
20 25 30

Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu

35

40

45

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser 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 Gly Gly Ser Gly Gly
 130 135 140

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

Phe Val Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile
 165 170 175

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

Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg
 195 200 205

Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser
 210 215 220

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

Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala
 245 250 255

<210> 51
 <211> 789
 <212> DNA
 <213> Artificial

<220>
 <223> scFv peptide

<220>
 <221> CDS

<222> (1)..(789)

<400> 51

atg gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg	48
Met Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro	
1 5 10 15	
ggt gaà tct ctg cgt atc tct tgc aaa ggt tct ggt tat agc atc tct	96
Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser	
20 25 30	
tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa	144
Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu	
35 40 45	
tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg	192
Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro	
50 55 60	
agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc	240
Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr	
65 70 75 80	
gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac	288
Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr	
85 90 95	
tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg	336
Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp	
100 105 110	
ggt cag ggc acc ctg gtg acc gtg agc agc ggt ggt ggc ggc agc ggt	384
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly	
115 120 125	
ggt ggc gga tct ggt ggt ggc ggc agc ggt ggt ggc gga tcc ggt ggt	432
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
130 135 140	
ggc ggc agc ggc ggc ggc ggc agc gat gtt gtg atg acc cag agc ccg	480
Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro	
145 150 155 160	
agc ttc ctg agc gcg ttc gtt ggt gac cgt atc acc att acc tgc cgc	528
Ser Phe Leu Ser Ala Phe Val Gly Asp Arg Ile Thr Ile Thr Cys Arg	
165 170 175	
gcc agc agc ggc atc agc cgc tat ctg gcg tgg tat cag caa gca ccg	576
Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala Trp Tyr Gln Gln Ala Pro	
180 185 190	
ggt aaa gca ccg aaa ctg ctg atc tat gct gca agc acc ctg caa acc	624
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Thr	
195 200 205	
ggc gtt ccg agc cgt ttt agc ggt agc ggc agc ggc acc gag ttc acc	672
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr	
210 215 220	
ctg acc atc aac agc ctg caa ccg gag gat ttt gcc acc tat tac tgc	720
Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys	
225 230 235 240	
caa cac ctg aat agc tat ccg ctg acc ttc ggt ggc ggc acc aaa gtg	768
Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val	
245 250 255	

gac atc aaa cgc gcg taa taa
 Asp Ile Lys Arg Ala
 260

789

<210> 52
 <211> 261
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 52

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

Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser
 20 25 30

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

Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro
 50 55 60

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

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

Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser 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 Gly Gly Ser Gly Gly
 130 135 140

Gly Gly Ser Gly Gly Gly Gly Ser Asp Val Val Met Thr Gln Ser Pro
 145 150 155 160

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

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

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

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 210 215 220

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

Gln His Leu Asn Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val
 245 250 255

Asp Ile Lys Arg Ala
 260

<210> 53

<211> 762

<212> DNA

<213> Artificial

<220>

<223> scFv peptide

<220>

<221> CDS

<222> (1)..(762)

<400> 53

atg gat gtt gtg atg acc cag agc ccg agc ttc ctg agc gcg ttc gtt 48
 Met Asp Val Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Phe Val
 1 5 10 15

ggt gac cgt atc acc att acc tgc cgc gcc agc agc ggc atc agc cgc 96
 Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg
 20 25 30

tat ctg gcg tgg tat cag caa gca ccg ggt aaa gca ccg aaa ctg ctg 144
 Tyr Leu Ala Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys Leu Leu
 35 40 45

atc tat gct gca agc acc ctg caa acc ggc gtt ccg agc cgt ttt agc 192
 Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser
 50 55 60

ggt agc ggc agc ggc acc gag ttc acc ctg acc atc aac agc ctg caa 240
 Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Gln
 65 70 75 80

ccg gag gat ttt gcc acc tat tac tgc caa cac ctg aat agc tat ccg 288
 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Pro
 85 90 95

ctg acc ttc ggt ggc ggc acc aaa gtg gac atc aaa cgc gcg agc ggt 336
 Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ser Gly
 100 105 110

ggt ggc ggc agc ggt ggt ggc gga tcc ggt ggt ggc ggc agc ggc ggc 384
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125

ggc ggc agc gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa 432
 Gly Gly Ser Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys

130 135 140
 aaa ccg ggt gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tat agc 480
 Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser
 145 150 155 160
 atc tct tct tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc 528
 Ile Ser Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly
 165 170 175
 ctg gaa tgg atg ggt aaa att gat ccg ggc gac agc tat att aac tac 576
 Leu Glu Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr
 180 185 190
 agc ccg agc ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att 624
 Ser Pro Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile
 195 200 205
 aac acc gct tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg 672
 Asn Thr Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala
 210 215 220
 atg tac tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat 720
 Met Tyr Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp
 225 230 235 240
 tac tgg ggt cag ggc acc ctg gtg acc gtg agc agc taa taa 762
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 245 250

 <210> 54
 <211> 252
 <212> PRT
 <213> Artificial

 <220>
 <223> Synthetic Construct

 <400> 54

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

 Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg
 20 25 30

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

 Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser
 50 55 60

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

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

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

116

100 105 110
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125
 Gly Gly Ser Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys
 130 135 140
 Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser
 145 150 155 160
 Ile Ser Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly
 165 170 175
 Leu Glu Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr
 180 185 190
 Ser Pro Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile
 195 200 205
 Asn Thr Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala
 210 215 220
 Met Tyr Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp
 225 230 235 240
 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 245 250

<210> 55
 <211> 777
 <212> DNA
 <213> Artificial

<220>
 <223> scFv peptide

<220>
 <221> CDS
 <222> (1)..(777)

<400> 55
 atg gat gtt gtg atg acc cag agc ccg agc ttc ctg agc gcg ttc gtt 48
 Met Asp Val Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Phe Val
 1 5 10 15
 ggt gac cgt atc acc att acc tgc cgc gcc agc agc ggc atc agc cgc 96
 Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg
 20 25 30
 tat ctg gcg tgg tat cag caa gca ccg ggt aaa gca ccg aaa ctg ctg 144
 Tyr Leu Ala Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys Leu Leu
 35 40 45
 atc tat gct gca agc acc ctg caa acc ggc gtt ccg agc cgt ttt agc 192

Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser	
50 55 60	
ggt agc ggc agc ggc acc gag ttc acc ctg acc atc aac agc ctg caa	240
Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Gln	
65 70 75 80	
ccg gag gat ttt gcc acc tat tac tgc caa cac ctg aat agc tat ccg	288
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Pro	
85 90 95	
ctg acc ttc ggt ggc ggc acc aaa gtg gac atc aaa cgc gcg agc ggt	336
Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ser Gly	
100 105 110	
ggt ggc ggc agc ggt ggt ggc gga tcc ggt ggt ggc ggc tcc ggt ggt	384
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly	
115 120 125	
ggc ggc agc ggc ggc ggc ggc agc gct gaa gtt caa ctt gtt gaa tct	432
Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Val Gln Leu Val Glu Ser	
130 135 140	
ggt gct gaa gtt aaa aaa ccg ggt gaa tct ctg cgt atc tct tgc aaa	480
Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys	
145 150 155 160	
ggt tct ggt tat agc atc tct tct tac tgg atc agc tgg gtt cgt cag	528
Gly Ser Gly Tyr Ser Ile Ser Ser Tyr Trp Ile Ser Trp Val Arg Gln	
165 170 175	
atg ccg ggc aag ggc ctg gaa tgg atg ggt aaa att gat ccg ggc gac	576
Met Pro Gly Lys Gly Leu Glu Trp Met Gly Lys Ile Asp Pro Gly Asp	
180 185 190	
agc tat att aac tac agc ccg agc ttt cag ggc cat gtt acc atc agc	624
Ser Tyr Ile Asn Tyr Ser Pro Ser Phe Gln Gly His Val Thr Ile Ser	
195 200 205	
gcc gat aaa agc att aac acc gct tac ctg caa tgg aac agc ctg aaa	672
Ala Asp Lys Ser Ile Asn Thr Ala Tyr Leu Gln Trp Asn Ser Leu Lys	
210 215 220	
gcg agc gac acc gcg atg tac tac tgt gcc cgt ggc ggt cgt gac ttc	720
Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Gly Gly Arg Asp Phe	
225 230 235 240	
ggt gat agc ttc gat tac tgg ggt cag ggc acc ctg gtg acc gtg agc	768
Gly Asp Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser	
245 250 255	
agc taa taa	777
Ser	

<210> 56

<211> 257

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 56

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

Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg
 20 25 30

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

Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser
 50 55 60

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

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

Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ser Gly
 100 105 110

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

Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Val Gln Leu Val Glu Ser
 130 135 140

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

Gly Ser Gly Tyr Ser Ile Ser Ser Tyr Trp Ile Ser Trp Val Arg Gln
 165 170 175

Met Pro Gly Lys Gly Leu Glu Trp Met Gly Lys Ile Asp Pro Gly Asp
 180 185 190

Ser Tyr Ile Asn Tyr Ser Pro Ser Phe Gln Gly His Val Thr Ile Ser
 195 200 205

Ala Asp Lys Ser Ile Asn Thr Ala Tyr Leu Gln Trp Asn Ser Leu Lys
 210 215 220

Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg Gly Gly Arg Asp Phe
 225 230 235 240

Gly Asp Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 245 250 255

Ser

<210> 57
 <211> 792
 <212> DNA
 <213> Artificial

<220>
 <223> scFv peptide

<220>
 <221> CDS
 <222> (1)..(792)

<400> 57
 atg gat gtt gtg atg acc cag agc ccg agc ttc ctg agc gcg ttc gtt 48
 Met Asp Val Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Phe Val
 1 5 10 15
 ggt gac cgt atc acc att acc tgc cgc gcc agc agc ggc atc agc cgc 96
 Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg
 20 25 30
 tat ctg gcg tgg tat cag caa gca ccg ggt aaa gca ccg aaa ctg ctg 144
 Tyr Leu Ala Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys Leu Leu
 35 40 45
 atc tat gct gca agc acc ctg caa acc ggc gtt ccg agc cgt ttt agc 192
 Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser
 50 55 60
 ggt agc ggc agc ggc acc gag ttc acc ctg acc atc aac agc ctg caa 240
 Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Gln
 65 70 75 80
 ccg gag gat ttt gcc acc tat tac tgc caa cac ctg aat agc tat ccg 288
 Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Pro
 85 90 95
 ctg acc ttc ggt ggc ggc acc aaa gtg gac atc aaa cgc gcg agc ggt 336
 Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ser Gly
 100 105 110
 ggt ggc ggc agc ggt ggt ggc gga tct ggt ggt ggc ggc agc ggt ggt 384
 Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
 115 120 125
 ggc gga tcc ggt ggt ggc ggc agc ggc ggc ggc ggc agc gct gaa gtt 432
 Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Glu Val
 130 135 140
 caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg ggt gaa tct ctg 480
 Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu
 145 150 155 160
 cgt atc tct tgc aaa ggt tct ggt tat agc atc tct tct tac tgg atc 528
 Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser Ser Tyr Trp Ile
 165 170 175
 agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa tgg atg ggt aaa 576
 Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Lys
 180 185 190
 att gat ccg ggc gac agc tat att aac tac agc ccg agc ttt cag ggc 624
 Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro Ser Phe Gln Gly

195 200 205
 cat gtt acc atc agc gcc gat aaa agc att aac acc gct tac ctg caa 672
 His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr Ala Tyr Leu Gln
 210 215 220
 tgg aac agc ctg aaa gcg agc gac acc gcg atg tac tac tgt gcc cgt 720
 Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
 225 230 235 240
 ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg ggt cag gcc acc 768
 Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp Gly Gln Gly Thr
 245 250 255
 ctg gtg acc gtg agc agc taa taa 792
 Leu Val Thr Val Ser Ser
 260

<210> 58
 <211> 262
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 58

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

Gly Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg
 20 25 30

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

Ile Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser
 50 55 60

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

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

Leu Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ser Gly
 100 105 110

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

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ala Glu Val
 130 135 140

Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu

145 150 155 160

Arg Ile Ser Cys Lys Gly Ser Gly Tyr Ser Ile Ser Ser Tyr Trp Ile
165 170 175

Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met Gly Lys
180 185 190

Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro Ser Phe Gln Gly
195 200 205

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

Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys Ala Arg
225 230 235 240

Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp Gly Gln Gly Thr
245 250 255

Leu Val Thr Val Ser Ser
260

<210>	59
<211>	837
<212>	DNA
<213>	Artificial

<220>
<223> scFv peptide

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<220>
<221> CDS
<222> (1)..(837)
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<400> 59
atg aaa tac ctg ctg ccg acc gct gct gct ggt ctg ctg ctc ctc gct      48
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1          5              10              15
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gcc cag ccg gcg atg gcc gct gaa gtt caa ctt gtt gaa tct ggt gct 96
Ala Gln Pro Ala Met Ala Ala Glu Val Gln Leu Val Glu Ser Gly Ala
20 25 30

gaa gtt aaa aaa cgg ggt gaa tct ctg cgt atc tct tgc aaa ggt tct 144
Glu Val Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser
35 40 45

ggt tgc atc atc tct tct tac tgg atc agc tgg gtt cgt cag atg ccg 192
Gly Cys Ile Ile Ser Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro
50 55 60

ggc aag ggc ctg gaa tgg atg ggt aaa att gat ccg ggc gac agc tat 240
Gly Lys Gly Leu Glu Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr
65 70 75 80

att aac tac agc ccg agc ttt cag ggc cat gtt acc atc agc gcc gat 288

122

Ile Asn Tyr Ser Pro Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp
85 90 95

aaa agc att aac acc gct tac ctg caa tgg aac agc ctg aaa gcg agc 336
Lys Ser Ile Asn Thr Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser
100 105 110

gac acc gcg atg tac tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat 384
Asp Thr Ala Met Tyr Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp
115 120 125

agc ttc gat tac tgg ggt cag ggc acc ctg gtg acc gtg agc agc ggt 432
Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
130 135 140

ggt ggc ggc agc ggt ggt ggc ggc agc ggc ggc ggc agc gat gtt 480
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Val
145 150 155 160

gtg atg acc cag agc ccg agc ttc ctg agc gcg ttc gtt ggt gac cgt 528
Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg
165 170 175

atc acc att acc tgc cgc gcc agc agc ggc atc agc cgc tat ctg gcg 576
Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala
180 185 190

tgg tat cag caa gca ccg ggt aaa gca ccg aaa ctg ctg atc tat gct 624
Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
195 200 205

gca agc acc ctg caa acc ggc gtt ccg agc cgt ttt agc ggt agc ggc 672
Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
210 215 220

agc ggc acc gag ttc acc ctg acc atc aac agc ctg caa ccg gag gat 720
Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp
225 230 235 240

ttt gcc acc tat tac tgc caa cac ctg aat agc tat ccg ctg acc ttc 768
Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe
245 250 255

ggt ggc ggc acc aaa gtg gac atc aaa cgc gcg gcc gca ctc gag cac 816
Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ala Ala Leu Glu His
260 265 270

cac cac cac cac cac taa taa 837
His His His His His
275

<210> 60
<211> 277
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 60

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Ala Glu Val Gln Leu Val Glu Ser Gly Ala
20 25 30

Glu Val Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser
35 40 45

Gly Cys Ile Ile Ser Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro
50 55 60

Gly Lys Gly Leu Glu Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr
65 70 75 80

Ile Asn Tyr Ser Pro Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp
85 90 95

Lys Ser Ile Asn Thr Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser
100 105 110

Asp Thr Ala Met Tyr Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp
115 120 125

Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
130 135 140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val
145 150 155 160

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

Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala
180 185 190

Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
195 200 205

Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
210 215 220

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

Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe
245 250 255

Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ala Ala Leu Glu His
260 265 270

His His His His His
275

<210> 61
 <211> 837
 <212> DNA
 <213> Artificial
 <220>
 <223> scFv peptide

<220>
 <221> CDS
 <222> (1)..(837)

<400> 61
 atg aaa tac ctg ctg ccg acc gct gct gct ggt ctg ctg ctc ctc gct 48
 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15
 gcc cag ccg gcg atg gcc gct gaa gtt caa ctt gtt gaa tct ggt gct 96
 Ala Gln Pro Ala Met Ala Ala Glu Val Gln Leu Val Glu Ser Gly Ala
 20 25 30
 gaa gtt aaa aaa ccg ggt gaa tct ctg cgt atc tct tgc aaa ggt tct 144
 Glu Val Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser
 35 40 45
 ggt tat atc atc tct tct tac tgg atc agc tgg gtt cgt cag atg ccg 192
 Gly Tyr Ile Ile Ser Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro
 50 55 60
 ggc aag ggc ctg gaa tgg atg ggt aaa att gat ccg ggc gac agc tat 240
 Gly Lys Gly Leu Glu Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr
 65 70 75 80
 att aac tac agc ccg agc ttt cag ggc cat gtt acc atc agc gcc gat 288
 Ile Asn Tyr Ser Pro Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp
 85 90 95
 aaa agc att aac acc gct tac ctg caa tgg aac agc ctg aaa gcg agc 336
 Lys Ser Ile Asn Thr Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser
 100 105 110
 gac acc gcg atg tac tac tgt gcc cgt ggc ggt cgt gac ttc ggt gat 384
 Asp Thr Ala Met Tyr Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp
 115 120 125
 agc ttc gat tac tgg ggt cag ggc acc ctg gtg acc gtg agc agc ggt 432
 Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
 130 135 140
 ggt ggc ggc agc ggt ggt ggc ggc agc ggc ggc ggc agc gat gtt 480
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val
 145 150 155 160
 gtg atg acc cag agc ccg agc ttc ctg agc gcg ttc gtt ggt gac cgt 528
 Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg
 165 170 175
 atc acc att acc tgc cgc gcc agc agc ggc atc agc cgc tat ctg gcg 576
 Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala
 180 185 190
 tgg tat cag caa gca ccg ggt aaa gca ccg aaa ctg ctg atc tat gct 624
 Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala

195 200 205

gca agc acc ctg caa acc ggc gtt ccg agc cgt ttt agc ggt agc ggc 672
 Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 210 215 220

agc ggc acc gag ttc acc ctg acc atc aac agc ctg caa ccg gag gat 720
 Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp
 225 230 235 240

ttt gcc acc tat tac tgc caa cac ctg aat agc tat ccg ctg acc ttc 768
 Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe
 245 250 255

ggt ggc ggc acc aaa gtg gac atc aaa cgc gcg gcc gca ctc gag cac 816
 Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ala Ala Leu Glu His
 260 265 270

cac cac cac cac cac taa taa 837
 His His His His His
 275

<210> 62
 <211> 277
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 62

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
 1 5 10 15

Ala Gln Pro Ala Met Ala Ala Glu Val Gln Leu Val Glu Ser Gly Ala
 20 25 30

Glu Val Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser
 35 40 45

Gly Tyr Ile Ile Ser Ser Tyr Trp Ile Ser Trp Val Arg Gln Met Pro
 50 55 60

Gly Lys Gly Leu Glu Trp Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr
 65 70 75 80

Ile Asn Tyr Ser Pro Ser Phe Gln Gly His Val Thr Ile Ser Ala Asp
 85 90 95

Lys Ser Ile Asn Thr Ala Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser
 100 105 110

Asp Thr Ala Met Tyr Tyr Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp
 115 120 125

Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly

130 135 140
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Val
 145 150 155 160
 Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Phe Val Gly Asp Arg
 165 170 175
 Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg Tyr Leu Ala
 180 185 190
 Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
 195 200 205
 Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
 210 215 220
 Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro Glu Asp
 225 230 235 240
 Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Pro Leu Thr Phe
 245 250 255
 Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala Ala Ala Leu Glu His
 260 265 270
 His His His His His
 275

<210> 63
 <211> 363
 <212> DNA
 <213> Artificial

<220>
 <223> Heavy chain of scFv peptide

<220>
 <221> CDS
 <222> (1)..(363)

<400> 63
 gct gaa gtt caa ctt gtt gaa tct ggt gct gaa gtt aaa aaa ccg ggt 48
 Ala Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly
 1 5 10 15
 gaa tct ctg cgt atc tct tgc aaa ggt tct ggt tgc atc atc tct tct 96
 Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser Ser
 20 25 30
 tac tgg atc agc tgg gtt cgt cag atg ccg ggc aag ggc ctg gaa tgg 144
 Tyr Trp Ile Ser Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp
 35 40 45
 atg ggt aaa att gat ccg ggc gac agc tat att aac tac agc ccg agc 192

Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro Ser
50 55 60

ttt cag ggc cat gtt acc atc agc gcc gat aaa agc att aac acc gct 240
Phe Gln Gly His Val Thr Ile Ser Ala Asp Lys Ser Ile Asn Thr Ala
65 70 75 80

tac ctg caa tgg aac agc ctg aaa gcg agc gac acc gcg atg tac tac 288
Tyr Leu Gln Trp Asn Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr
85 90 95

tgt gcc cgt ggc ggt cgt gac ttc ggt gat agc ttc gat tac tgg ggt 336
Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp Gly
100 105 110

cag ggc acc ctg gtg acc gtg agc agc 363
Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 64
<211> 121
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 64

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

Glu Ser Leu Arg Ile Ser Cys Lys Gly Ser Gly Cys Ile Ile Ser Ser
20 25 30

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

Met Gly Lys Ile Asp Pro Gly Asp Ser Tyr Ile Asn Tyr Ser Pro Ser
50 55 60

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

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

Cys Ala Arg Gly Gly Arg Asp Phe Gly Asp Ser Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 65
<211> 327
<212> DNA
<213> Artificial

<220>

<223> Light chain from scFv peptide

 $\langle 220 \rangle$

<221> CDS

<222> (1) .. (327)

<400> 65

gat gtt gtg atg acc cag agc ccg agc ttc ctg agc gcg ttc gtt ggt 48
Asp Val Val Met Thr Gln Ser Pro Ser Phe Leu Ser Ala Phe Val Gly
1 5 10 15

gac cgt atc acc att acc tgc cgc gcc agc agc ggc atc agc cgc tat 96
Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg Tyr
20 25 30

ctg gcg tgg tat cag caa gca ccg ggt aaa gca ccg aaa ctg ctg atc 144
Leu Ala Trp Tyr Gln Gln Ala Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

tat gct gca agc acc ctg caa acc ggc gtt ccg agc cgt ttt agc ggt 192
Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

agc ggc agc ggc acc gag ttc acc ctg acc atc aac agc ctg caa ccg 240
 Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro
 65 70 75 80

gag gat ttt gcc acc tat tac tgc caa cac ctg aat agc tat ccg ctg 288
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His Leu Asn Ser Tyr Pro Leu
85 90 95

acc ttc ggt ggc ggc acc aaa gtg gac atc aaa cgc gcg 327
Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala
100 105

<210> 66

<211> 109

<212> PRT

<213> Artificial

 $\langle 220 \rangle$

<223> Synthetic Construct

<400> 66

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

Asp Arg Ile Thr Ile Thr Cys Arg Ala Ser Ser Gly Ile Ser Arg Tyr
20 25 30

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

Tyr Ala Ala Ser Thr Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro

Thr Phe Gly Gly Gly Thr Lys Val Asp Ile Lys Arg Ala
100 105

<220>
<223> pelB signal sequence

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<400> 67
atg aaa tac ctg ctg ccg acc gct gct gct ggt ctg ctg ctc ctc gct      48
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1          5          10          15
```

gcc cag ccg gcg atg gcc 66
Ala Gln Pro Ala Met Ala
20

<220>
<223> Synthetic Construct

<400> 68

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala
20

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<210> 69
<211> 14
<212> PRT
<213> Candida albicans
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<400> 69

Asn Lys Ile Leu Lys Val Ile Arg Lys Asn Ile Val Lys Lys
1 5 10

<210>	70
<211>	15
<212>	PRT

<213> Artificial

<220>

<223> Scrambled peptide

<400> 70

Ser	Phe	Lys	Trp	Gly	Val	Thr	Thr	Ser	Leu	Ser	Tyr	Phe	Pro	Lys
1				5					10					15