

<110> LG CHEM, LTD.
 <120> Polypeptide specific to Mucin1 and use thereof
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 <150> KR10-2020-0183768
 <151> 2020-12-24
 <150> KR10-2021-0137757
 <151> 2021-10-15
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 Gly Phe Thr Val Ser Ser Asn Tyr
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 <211> 7
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 <223> 2445_1F09 HCDR2
 <400> 2
 Ile Tyr Ser Gly Gly Ser Thr
 1 5
 <210> 3
 <211> 10
 <212> PRT
 <213> Artificial Sequence
 <220>

<223> 2445_1F09 HCDR3

<400> 3

Asp Arg Gly Trp Asn His Gly Met Asp Val
1 5 10

<210> 4

<211> 8

<212> PRT

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<220>

<223> 2445_1F09 LCDR1

<400> 4

Ser Ser Glu Val Gly Ser Arg Tyr
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<210> 5

<211> 3

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<213> Artificial Sequence

<220>

<223> 2445_1F09 LCDR2

<400> 5

Lys Asn Asp
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<210> 6

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 2445_1F09 LCDR3

<400> 6

Ala Ala Trp Asp Asp Ser Leu Asn Gly Tyr Val
1 5 10

<210> 7
 <211> 118
 <212> PRT
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<220>
 <223> 2445_1F09 VH

<400> 7
 Glu Val Gln Leu Leu Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser Asn
 20 25 30
 Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Val Ile Tyr Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Asp Arg Gly Trp Asn His Gly Met Asp Val Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser
 115

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 <223> 2445_1F09 VL

<400> 8
 Gln Ser Gly Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Ser Gly Gly Ser Ser Glu Val Gly Ser Arg
 20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Arg Leu Leu
35 40 45

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

Gly Ser Lys Ser Gly Ser Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

Asn Gly Tyr Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 9
<211> 243
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<220>
<223> 2445_1F09 scFv

<400> 9
Glu Val Gln Leu Leu Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

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

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

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

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

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

Arg Asp Arg Gly Trp Asn His Gly Met Asp Val Trp Gly Gln Gly Thr
100 105 110

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

Gly Gly Gly Ala Ser Gln Ser Gly Leu Thr Gln Pro Pro Ser Ala Ser
130 135 140

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

Glu Val Gly Ser Arg Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr
165 170 175

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

Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Ser Ser Ala Ser Leu Ala
195 200 205

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

Trp Asp Asp Ser Leu Asn Gly Tyr Val Phe Gly Thr Gly Thr Lys Leu
225 230 235 240

Thr Val Leu

<210> 10
<211> 729
<212> DNA
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<220>
<223> 2445_1F09 scFv

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ccagggaagg ggctggagtg ggtctcagtt atttatagcg gtggtagcac atattacgca 180
gactccgtga agggccgatt caccatctcc agagacaatt ccaagaacac gctgtatctt 240
caaatgaaca gcctgagagc cgaggacacg gccgtgtatt actgtgcgag agatcgcggc 300
tggaaccacg gtatggacgt ctggggccag ggaaccctgg tcaccgtctc gagggtgga 360
ggcgggttcag gcggaggtgg ctctggcggg ggcgctagcc agtctgggct gactcagcca 420

ccctcagcgt ctgggacccc cgggcagagg gtcaccatct cttgttctgg gggcagctca	480
gaagtcggaa gtagatatgt gtcctggtac cagcaactcc caggaacggc cccagactc	540
ctcatctata agaatgatcg gcggccctca ggggtccctg accgattctc tggctccaag	600
tctggctcct cagcctccct ggccatcagt gggctccggt ccgaggatga ggctgattat	660
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accgtccta	729

<210> 11
 <211> 8
 <212> PRT
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<220>
 <223> 2447_2H08 HCDR1

<400> 11
 Gly Tyr Thr Phe Thr Asn Tyr Gly
 1 5

<210> 12
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_2H08 HCDR2

<400> 12
 Ile Ser Ala Tyr Asn Gly Asn Thr
 1 5

<210> 13
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_2H08 HCDR3

<400> 13
 Asp Pro His Ile Leu Thr Gly Tyr Tyr Arg Gly Gly Trp Phe Asp Pro
 1 5 10 15

<210> 14
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_2H08 LCDR1

<400> 14
 Ser Leu Arg Thr Ser Tyr
 1 5

<210> 15
 <211> 3
 <212> PRT
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<220>
 <223> 2447_2H08 LCDR2

<400> 15
 Gly Lys Thr
 1

<210> 16
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_2H08 LCDR3

<400> 16
 His Ser Arg Asp Ser Asn Asp Asn Tyr Leu Glu Val Val
 1 5 10

<210> 17

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

<220>
<223> 2447_2H08 VH

<400> 17
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
50 55 60
Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Pro His Ile Leu Thr Gly Tyr Tyr Arg Gly Gly Trp Phe
100 105 110
Asp Pro Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 18
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_2H08 VL

<400> 18
Ser Tyr Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
1 5 10 15
Thr Val Thr Ile Thr Cys Gln Gly Asp Ser Leu Arg Thr Ser Tyr Ala
20 25 30

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

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

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

Asp Glu Ala Glu Tyr Phe Cys His Ser Arg Asp Ser Asn Asp Asn Tyr
85 90 95

Leu Glu Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 19
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_2H08 scFv

<400> 19
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

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

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

Ala Arg Asp Pro His Ile Leu Thr Gly Tyr Tyr Arg Gly Gly Trp Phe
100 105 110

Asp Pro Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
115 120 125

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

<210> 20
 <211> 750
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2447_2H08 scFv

<400> 20
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 cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatggtaa cacaactat 180
 gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240
 atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagatccg 300
 catattttga ctggttatta taggggaggg tggttcgacc cctgggggca agggaccacg 360
 gtcaccgtct cgagtgggtg aggcggttca ggcggagggt gctctggcgg tggcgctagc 420
 tcctatgagc tgactcagga ccctgctgtg tctgtggcct tgggtcagac agtcaccatc 480

acgtgccaag gagacagcct cagaacctct tatgcaggct ggctccagca gaagccagga	540
caggcccctg tactcgtcct ctatggtaaa accagccggc cctcagggat cccagaccga	600
ttctctggct ccacctcagg aaacacagct tccttgacca tcactggggc tcaggcggag	660
gatgaggctg agtatttctg tcactcccgg gacagcaatg ataactatct agaggtggtt	720
ttcggcggag ggaccaagct gaccgtccta	750

<210> 21
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3A01 HCDR1

<400> 21
 Gly Phe Thr Phe Asp Asp Tyr Ala
 1 5

<210> 22
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3A01 HCDR2

<400> 22
 Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 23
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3A01 HCDR3

<400> 23

Asp Ile Ser Ser Gly Trp Tyr Pro Gly Thr Phe Asp Tyr
1 5 10

<210> 24
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A01 LCDR1

<400> 24
Ser Leu Arg Ser Tyr Tyr
1 5

<210> 25
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A01 LCDR2

<400> 25
Gly Lys Asn
1

<210> 26
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A01 LCDR3

<400> 26
Ser Ser Arg Asp Ser Ser Asp Asp Val Val
1 5 10

<210> 27
<211> 122
<212> PRT
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<220>

<223> 2447_3A01 VH

<400> 27

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

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

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

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

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

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

Ala Lys Asp Ile Ser Ser Gly Trp Tyr Pro Gly Thr Phe Asp Tyr Trp
100 105 110

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

<210> 28

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> 2447_3A01 VL

<400> 28

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

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

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

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

<210> 29
 <211> 244
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3A01 scFv

<400> 29
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Val Tyr Ala Asp Phe Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Ile Ser Ser Gly Trp Tyr Pro Gly Thr 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 Ala Ser Ser Tyr Glu Leu Thr Gln Asp
 130 135 140

Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln
 145 150 155 160
 Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro
 165 170 175
 Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser
 180 185 190
 Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser
 195 200 205
 Leu Thr Val Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
 210 215 220
 Ser Ser Arg Asp Ser Ser Asp Asp Val Val Phe Gly Gly Gly Thr Gln
 225 230 235 240
 Leu Thr Val Leu

<210> 30
 <211> 732
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> 2447_3A01 scFv

<400> 30
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 tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
 ccagggaagg gcctggagt ggtctcaggt attagttgga atagtggtag catagtctat 180
 gcggactttg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
 ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagatatt 300
 tcaagtggct ggtacccagg gacctttgac tactggggcc agggaaccct ggtcaccgtc 360
 tcgagtgggtg gaggcggttc aggcggaggt ggctctggcg gtggcgctag ctcctatgag 420
 ctgactcagg accctgctgt gtctgtggcc ttgggacaga cagtcaggat cacatgccaa 480
 ggagacagcc tcagaagcta ttatgcaagc tggtaccagc agaagccagg acaggcccct 540

gtacttgtca tctatggtaa aaacaaccgg ccctcaggga tcccagaccg attctctggc 600
tccagctcag gaaacacagc ttccttgacc gtcactgggg ctcaggcgga agacgaggct 660
gactattact gtagctcccg ggacagcagt gatgatgtgg tattcggcgg agggacccag 720
ctcaccgtcc ta 732

<210> 31
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A08 HCDR1

<400> 31
Gly Tyr Thr Phe Thr Ser Tyr Gly
1 5

<210> 32
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A08 HCDR2

<400> 32
Ile Ser Ala Tyr Asn Gly Asn Thr
1 5

<210> 33
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A08 HCDR3

<400> 33
Asp Arg Ala Thr Ile Phe Gly Val Val Thr Pro Phe Asp Tyr
1 5 10

<210> 34
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A08 LCDR1

<400> 34
Ser Ile Arg Ser Tyr Ser
1 5

<210> 35
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A08 LCDR2

<400> 35
Gly Lys Asn
1

<210> 36
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A08 LCDR3

<400> 36
Asn Ser Arg Asp Ser Ser Gly Asn Arg Val Val
1 5 10

<210> 37
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A08 VH

<400> 37
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu
 50 55 60
 Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Arg Ala Thr Ile Phe Gly Val Val Thr Pro Phe Asp Tyr
 100 105 110
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 38
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3A08 VL

<400> 38
 Ser Tyr Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
 1 5 10 15
 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Ile Arg Ser Tyr Ser Ala
 20 25 30
 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Val Ile Tyr
 35 40 45
 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Val Ser Gly Ser
 50 55 60

Thr Ser Gly Asn Thr Ala Ser Leu Thr Val Thr Gly Ala Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn Arg
85 90 95

Val Val Phe Gly Gly Gly Thr Gln Leu Thr Val Leu
100 105

<210> 39
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A08 scFv

<400> 39
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

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

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

Ala Arg Asp Arg Ala Thr Ile Phe Gly Val Val Thr Pro Phe Asp Tyr
100 105 110

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

Gly Gly Gly Gly Ser Gly Gly Gly Ala Ser Ser Tyr Glu Leu Thr Gln
130 135 140

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

Gln Gly Asp Ser Ile Arg Ser Tyr Ser Ala Ser Trp Tyr Gln Gln Lys
 165 170 175
 Pro Gly Gln Ala Pro Arg Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro
 180 185 190
 Ser Gly Ile Pro Asp Arg Val Ser Gly Ser Thr Ser Gly Asn Thr Ala
 195 200 205
 Ser Leu Thr Val Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr
 210 215 220
 Cys Asn Ser Arg Asp Ser Ser Gly Asn Arg Val Val Phe Gly Gly Gly
 225 230 235 240
 Thr Gln Leu Thr Val Leu
 245

<210> 40
 <211> 738
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2447_3A08 scFv

<400> 40
 gaagtgcagc tggtgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggctc 60
 tcctgcaagg cttctggtta cacctttacc agctacggta tcagctgggt gcgacaggcc 120
 cctggacaag ggcttgagtg gatgggatgg atcagcgctt acaatggtaa cacaaactat 180
 gcacagaagc tccagggcag agtcaccatg accacagaca catccacgag cacagcctac 240
 atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagatcgg 300
 gctacgattt ttggagtggg taccctctt gactactggg gccaaaggaac cctggtcacc 360
 gtctcgagtg gtggaggcgg ttcaggcgga ggtggctctg gcggtggcgc tagctcctat 420
 gagctgactc aggaccccg cgtgtctgtg gccttgggac agacagtcag gatcacatgc 480
 cagggagaca gtattagaag ttattctgcc agctgggtacc agcagaagcc agggcaggcc 540
 cctcgccttg ttatctatgg taaaaacaac cggccctcag ggatcccaga ccgagtctct 600
 ggctccactt caggaaatac agcttccttg accgtcactg gggctcaggc ggaagatgag 660

gctgactatt actgtaactc ccgggacagc agtggttaacc gtgtggtatt cggcggaggg 720
 acccagctca ccgtccta 738

<210> 41
 <211> 8
 <212> PRT
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<220>
 <223> 2447_3A09 HCDR1

<400> 41
 Gly Phe Thr Phe Asp Asp Tyr Ala
 1 5

<210> 42
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3A09 HCDR2

<400> 42
 Ile Ser Trp Asn Ser Gly Ser Ile
 1 5

<210> 43
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3A09 HCDR3

<400> 43
 Asp Val Ser Ser Gly Trp Tyr Trp Tyr Ala Phe Asp Ile
 1 5 10

<210> 44
 <211> 6

<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A09 LCDR1

<400> 44
Ser Leu Arg Ser Tyr Tyr
1 5

<210> 45
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A09 LCDR2

<400> 45
Gly Lys Asn
1

<210> 46
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A09 LCDR3

<400> 46
Asn Ser Arg Asp Ser Gly Gly Ser Val Val
1 5 10

<210> 47
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A09 VH

<400> 47

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

<210> 48
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3A09 VL

<400> 48
 Ser Tyr Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
 1 5 10 15
 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
 20 25 30
 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45
 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Gly Arg Phe Ser Gly Ser
 50 55 60
 Ser Ser Gly Asn Thr Ala Ser Leu Thr Val Thr Gly Ala Gln Ala Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Gly Gly Ser Val
85 90 95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 49
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A09 scFv

<400> 49
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

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

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

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

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

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

Ala Lys Asp Val Ser Ser Gly Trp Tyr Trp Tyr Ala Phe Asp Ile 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 Ala Ser Ser Tyr Glu Leu Thr Gln Asp
130 135 140

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

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

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

Gly Ile Pro Gly Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser
195 200 205

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

Asn Ser Arg Asp Ser Gly Gly Ser Val Val Phe Gly Gly Gly Thr Lys
225 230 235 240

Leu Thr Val Leu

<210> 50
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> 2447_3A09 scFv

<400> 50
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggcaggctc cctgagactc 60
tcctgtgcag ccactggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
ccagggaagg gcctggagt ggtctcaggt attagttgga atagtggtag cataggctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggcctcgt attactgtgc aaaagatggt 300
agcagtggct ggtactggta tgcttttgat atctggggcc aaggaaccct ggtcaccgtc 360
tcgagtgggtg gaggcggttc aggcggaggt ggctctggcg gtggcgctag ctcctatgag 420
ctgactcagg accctgctgt gtctgtggcc ttgggacaga cagtcaggat cacatgccaa 480
ggagacagcc tcagaagcta ttatgcaagc tggtaccagc agaagccagg acaggcccct 540
gtacttgtca tctatggtaa aaacaaccgg ccctcaggga tcccaggccg attctctggc 600
tccagctcag gaaacacagc ttccttgacc gtcactgggg ctcaggcgga agatgaggct 660
gactattact gtaattcccg ggacagcggg ggttctgtgg ttttcggcgg agggaccaag 720

ctgaccgtcc ta

732

<210> 51
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A12 HCDR1

<400> 51
Gly Tyr Thr Phe Thr Ser Tyr Gly
1 5

<210> 52
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A12 HCDR2

<400> 52
Ile Ser Ala Tyr Asn Gly Asn Thr
1 5

<210> 53
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3A12 HCDR3

<400> 53
Asp Pro His Ile Leu Thr Gly Tyr Tyr Arg Gly Gly Trp Phe Asp Pro
1 5 10 15

<210> 54
<211> 6
<212> PRT

<213> Artificial Sequence

<220>

<223> 2447_3A12 LCDR1

<400> 54

Ser Leu Arg Ser Tyr Tyr
1 5

<210> 55

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> 2447_3A12 LCDR2

<400> 55

Gly Lys Asn
1

<210> 56

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 2447_3A12 LCDR3

<400> 56

Asn Ser Arg Asp Ser Ser Gly Asn His Arg Val
1 5 10

<210> 57

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> 2447_3A12 VH

<400> 57

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

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

<210> 58
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3A12 VL

<400> 58
Ser Tyr Glu Leu Thr Gln Asp Pro Ala Val Ser Val Val Leu Gly Gln
1 5 10 15
Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
20 25 30
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45
Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60
Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
65 70 75 80
Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His

	85	90	95
Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu			
	100	105	
<210>	59		
<211>	248		
<212>	PRT		
<213>	Artificial Sequence		
<220>			
<223>	2447_3A12 scFv		
<400>	59		
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala			
1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr			
	20	25	30
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met			
	35	40	45
Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Leu			
	50	55	60
Arg Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr			
	65	70	75
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys			
	85	90	95
Ala Arg Asp Pro His Ile Leu Thr Gly Tyr Tyr Arg Gly Gly Trp Phe			
	100	105	110
Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly			
	115	120	125
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ser Ser Tyr Glu Leu			
	130	135	140
Thr Gln Asp Pro Ala Val Ser Val Val Leu Gly Gln Thr Val Arg Ile			
	145	150	155
Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln			
	165	170	175
Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn			

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

<210> 60
 <211> 744
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2447_3A12 scFv

<400> 60
 gaagtgcagc tggatgcagtc tggagctgag gtgaagaagc ctggggcctc agtgaaggctc 60
 tcctgcaagg cttctgggta cacctttacc agctatggta tcagctgggt gcgacaggcc 120
 cctggacaag ggcttgagt gatgggatgg atcagcgctt acaatggtaa cacaaactat 180
 gcacagaagc tccggggcag agtcaccatg accacagaca catccacgag cacagcctac 240
 atggagctga ggagcctgag atctgacgac acggccgtgt attactgtgc gagagatccg 300
 catattttga ctggttatta taggggaggg tggttcgacc cctggggcca gggcacctg 360
 gtcaccgtct cgagtgggtg aggcgggttca ggcggaggtg gctctggcgg tggcgctagc 420
 tcctatgagc tgactcagga ccctgctgtg tctgtggtct tgggacagac agtcaggatc 480
 acatgccaag gagacagcct cagaagctat tatgcaagct ggtaccagca gaagccagga 540
 caggcccctg tacttgtcat ctatggtaaa aacaaccggc cctcagggat cccagaccga 600
 ttctctggct ccagctcagg aaacacagct tccttgacca tcaactggggc tcaggcggaa 660
 gatgaggctg actattactg taactcccgg gacagcagtg gtaaccatcg tgtattcggc 720
 ggagggacca agctgaccgt ccta 744

<210> 61
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3B07 HCDR1

<400> 61
Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 62
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3B07 HCDR2

<400> 62
Thr Ser Trp Asp Gly Gly Ser Thr
1 5

<210> 63
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3B07 HCDR3

<400> 63
Asp His Ser Ser Gly Trp Tyr Asn Gly Gly
1 5 10

<210> 64
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> 2447_3B07 LCDR1

<400> 64
Ser Leu Arg Ser Tyr Tyr
1 5

<210> 65
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3B07 LCDR2

<400> 65
Gly Lys Asn
1

<210> 66
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3B07 LCDR3

<400> 66
Asn Ser Arg Asp Ser Ser Gly Asn His Val Val
1 5 10

<210> 67
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3B07 VH

<400> 67
Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Val Gln Pro Gly Gly
1 5 10 15

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

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

<210> 68
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3B07 VL

<400> 68
 Ser Tyr Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln
 1 5 10 15
 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
 20 25 30
 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45
 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
 50 55 60
 Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
 65 70 75 80
 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His
 85 90 95
 Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100

105

<210> 69
 <211> 245
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3B07 scFv

<400> 69
 Gln Val Gln Leu Val Glu Ser Gly Gly Val Val Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Glu Trp Val
 35 40 45
 Ser Leu Thr Ser Trp Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Ala Lys Asp His Ser Ser Gly Trp Tyr Asn Gly Gly Met Asp Val Trp
 100 105 110
 Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
 115 120 125
 Gly Gly Gly Ser Gly Gly Gly Ala Ser Ser Tyr Glu Leu Thr Gln Asp
 130 135 140
 Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln
 145 150 155 160
 Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro
 165 170 175
 Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser
 180 185 190
 Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser

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

<210> 70
 <211> 735
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2447_3B07 scFv

<400> 70
 caggtgcagc tgggtggagtc tggggggagtc gtggtacagc ctgggggggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatgcc a tgactgggt ccgtcaagct 120
 ccggggaggg gtctggagtg ggtctctctt actagttggg atggtggtag cacatactat 180
 gcagactctg tgaagggtcg attcaccatc tccagagaca acagcaaaaa ctccctgtat 240
 ctgcaaatga acagtctgag agctgaggac accgccttgt attactgtgc aaaagatcat 300
 agcagcggct ggtacaacgg gggatatggac gtctggggcc aagggacaat ggtcaccgtc 360
 tcgagtgggtg gaggcggttc aggcggaggt ggctctggcg gtggcgctag ctcttatgag 420
 ctgactcagg accctgctgt gtctgtggcc ttgggacaga cagtcaggat cacatgccaa 480
 ggagacagcc tcagaagcta ttatgcaagc tggtaccagc agaagccagg acaggcccct 540
 gtacttgtca tctatggtaa aaacaaccgg ccctcagga tcccagaccg attctctggc 600
 tccagctcag gaaacacagc ttccttgacc atcactgggg ctgaggcgga agatgaggct 660
 gactattact gtaactcccg ggacagcagt ggtaaccatg tggatttcgg cggagggacc 720
 aagctgaccg tccta 735

<210> 71

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

<220>
<223> 2447_3C08 HCDR1

<400> 71
Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 72
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3C08 HCDR2

<400> 72
Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 73
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3C08 HCDR3

<400> 73
Asp Arg Gly Ser Gly Tyr Glu Gly Asn Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 74
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3C08 LCDR1

<400> 74
Ser Leu Arg Ser Tyr Tyr
1 5

<210> 75
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3C08 LCDR2

<400> 75
Gly Lys Asn
1

<210> 76
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3C08 LCDR3

<400> 76
Asn Ser Arg Asp Ser Ser Gly Asn His Tyr Val
1 5 10

<210> 77
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3C08 VH

<400> 77
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

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

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

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

<210> 78
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3C08 VL

<400>	78														
Ser	Tyr	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln
1				5					10					15	
Thr	Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala
			20					25					30		
Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr
		35					40					45			
Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Thr
	50					55					60				
Thr	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu
	65				70					75					80
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Asn	Ser	Arg	Asp	Ser	Ser	Gly	Asn	His
			85						90					95	
Tyr	Val	Phe	Gly	Thr	Gly	Thr	Lys	Val	Thr	Val	Leu				
		100					105								

<210> 79
 <211> 247
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3C08 scFv

<400> 79
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30
 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Arg Gly Ser Gly Tyr Glu Gly Asn Tyr Tyr Gly Met Asp
 100 105 110
 Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125
 Ser Gly Gly Gly Gly Ser Gly Gly Gly Ala Ser Ser Tyr Glu Leu Thr
 130 135 140
 Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr
 145 150 155 160
 Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Gln Gln
 165 170 175
 Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg
 180 185 190
 Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Thr Thr Ser Gly Asn Thr
 195 200 205
 Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr

210	215	220
Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn His Tyr Val Phe Gly Thr		
225	230	235
		240

Gly Thr Lys Val Thr Val Leu
245

<210> 80
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> 2447_3C08 scFv

<400> 80
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggggtc cctgagactc 60
tcctgtgcag cctctggatt cacctttgat gattatgcca tgcactgggt ccggcaagct 120
ccagggaagg gcctggagtg ggtctcaggt attagttaga atagtggtag cataggctat 180
gcggactctg tgaagggccg attcaccatc tccagagaca acgccaagaa ctccctgtat 240
ctgcaaatga acagtctgag agctgaggac acggccttgt attactgtgc aaaagatagg 300
ggtagtggct acgaaggaaa ctactacggc atggacgtct ggggccaagg aaccctggctc 360
accgtctcga gtggtggagg cggttcaggc ggaggtggct ctggcggtgg cgctagctcc 420
tatgagctga ctcaggaccc tgctgtgtct gtggccttgg gacagacagt caggatcaca 480
tgccaaggag acagcctcag aagctattat gcaagctggc accagcagaa gccaggacag 540
gcccctgtac ttgtcatcta tggtaaaaac aaccggccct cagggatccc agaccgattc 600
tctggtacca cctcaggaaa cacagcctcc ttgaccatca ctggggctca ggcggaagat 660
gaggctgact attactgtaa ctcccgggac agcagtggta accattatgt cttcggaact 720
gggaccaagg tcaccgtcct a 741

<210> 81
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> 2447_3H02 HCDR1

<400> 81

Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 82

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> 2447_3H02 HCDR2

<400> 82

Ile Ser Trp Asp Ser Gly Ser Ile
1 5

<210> 83

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> 2447_3H02 HCDR3

<400> 83

Asp Val Ser Ser Gly Trp Tyr Trp Tyr Ala Phe Asp Ile
1 5 10

<210> 84

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> 2447_3H02 LCDR1

<400> 84

Ile Leu Arg Ser Tyr Tyr
1 5

<210> 85
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3H02 LCDR2

<400> 85
Gly Lys Asn
1

<210> 86
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3H02 LCDR3

<400> 86
Asn Ser Arg Asp Ser Ser Gly Asn Arg Val Val
1 5 10

<210> 87
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3H02 VH

<400> 87
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

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

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

Ser Gly Ile Ser Trp Asp Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val

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

<210> 88
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3H02 VL

<400>	88														
Ser	Tyr	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln
1				5					10					15	
Thr	Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ile	Leu	Arg	Ser	Tyr	Tyr	Ala
			20					25					30		
Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr
		35					40					45			
Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Ser	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu
65					70					75					80
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Asn	Ser	Arg	Asp	Ser	Ser	Gly	Asn	Arg
			85						90					95	
Val	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu				
			100					105							

<210> 89
 <211> 245
 <212> PRT

<213> Artificial Sequence

<220>

<223> 2447_3H02 scFv

<400> 89

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

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

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

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

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

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

Ala Lys Asp Val Ser Ser Gly Trp Tyr Trp Tyr Ala Phe Asp Ile 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 Ala Ser Ser Tyr Glu Leu Thr Gln Asp
130 135 140

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

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

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

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

Leu Thr Ile Thr Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
210 215 220

Asn Ser Arg Asp Ser Ser Gly Asn Arg Val Val Phe Gly Gly Gly Thr

225 230 235 240

<210>	90
<211>	735
<212>	DNA
<213>	Artificial Sequence

<400>	90	
gaggtgcagc	tgttggagtc	tgggggaggc
ttggtacagc	ctggcaggtc	cctgagactc
60		
tcctgtgcag	cctctggatt	cacctttgat
gattatgcca	tgcactgggt	ccggcaagct
120		
ccaggggaagg	gcctggagtg	ggctctcaggt
attagttggg	atagtggtag	cataggctat
180		
gcggactctg	tgaagggccg	attcaccatc
tccagagaca	acgccaagaa	ctccctgtat
240		
ctgcaaatga	acagtctgag	agctgaggac
acggccttgt	attactgtgc	aaaagatgtt
300		
agcagtggct	ggtactggta	tgcttttgat
atctggggcc	agggaaccct	ggtcaccgtc
360		
tcgagtggtg	gaggcggttc	aggcggagggt
ggctctggcg	gtggcgctag	ctcctatgag
420		
ctgactcagg	accctgctgt	gtctgtggcc
ttgggacaga	cagtcaggat	cacatgccaa
480		
ggagacatcc	tcagaagtta	ttatgcaagt
tgggtaccagc	agaagccagg	acaggcccct
540		
gtacttgtca	tttatggtaa	aaacaaccgg
ccctcaggga	tcccagaccg	attctctggc
600		
tccagctcag	gaaacacagc	ttccttgacc
atcactgggg	ctcaggcgga	agatgaggct
660		
gactattact	gtaactcccc	ggacagcagt
ggtaaccgtg	tgggtattcg	cggagggacc
720		
aagctgaccg	tccta	
735		

<400> 91
Gly Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 92
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3H08 HCDR2

<400> 92
Ile Ser Trp Asn Ser Gly Ser Ile
1 5

<210> 93
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3H08 HCDR3

<400> 93
Asp Arg Ser Ser Gly Trp Tyr Thr Gly Ser Phe Asp Tyr
1 5 10

<210> 94
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3H08 LCDR1

<400> 94
Ser Leu Arg Ser Tyr Tyr
1 5

<210> 95

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

<220>
<223> 2447_3H08 LCDR2

<400> 95
Gly Lys Asn
1

<210> 96
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3H08 LCDR3

<400> 96
Gln Ser Arg Asp Ser Ser Asp Asn Arg Val Leu
1 5 10

<210> 97
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> 2447_3H08 VH

<400> 97
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15

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

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

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

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

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

<210> 98
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 2447_3H08 VL

<400>	98														
Ser	Tyr	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln
1				5					10					15	
Thr	Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala
			20					25					30		
Ser	Trp	Tyr	Arg	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr
		35					40					45			
Gly	Lys	Asn	Asn	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser
	50					55					60				
Ser	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ile	Gly	Ala	Gln	Ala	Glu
65					70				75						80
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Arg	Asp	Ser	Ser	Asp	Asn	Arg
				85					90					95	
Val	Leu	Phe	Gly	Gly	Gly	Thr	Lys	Val	Thr	Val	Leu				
			100					105							

<210> 99
 <211> 245
 <212> PRT
 <213> Artificial Sequence

<220>

<223> 2447_3H08 scFv

<400> 99

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30
Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Asp Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asp Arg Ser Ser Gly Trp Tyr Thr Gly 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 Ala Ser Ser Tyr Glu Leu Thr Gln Asp
130 135 140
Pro Ala Val Ser Val Ala Leu Gly Gln Thr Val Arg Ile Thr Cys Gln
145 150 155 160
Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser Trp Tyr Arg Gln Lys Pro
165 170 175
Gly Gln Ala Pro Val Leu Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser
180 185 190
Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser
195 200 205
Leu Thr Ile Ile Gly Ala Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
210 215 220
Gln Ser Arg Asp Ser Ser Asp Asn Arg Val Leu Phe Gly Gly Gly Thr
225 230 235 240
Lys Val Thr Val Leu

<210> 100
 <211> 735
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 2447_3H08 scFv

<400> 100
 gaggtgcagc tggttgagtc tgggggaggc ttggtacagc ctggcaggtc cctgagactc 60
 tcctgtgcag cctctggatt cacctttgat gattatgcc a tgcaactgggt ccggcaagct 120
 ccagggaagg gcctggagtg ggtctcaggt attagttaga atagtggtag catagactat 180
 gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240
 ctgcaaatga acagcctgag agctgaggac acagctgtgt actactgtgc gagagatcgg 300
 agtagtggct ggtacacggg gtcctttgac tactggggcc agggcaccct ggtcaccgtc 360
 tcgagtgggtg gaggcgggtc aggcggaggt ggctctggcg gtggcgctag ctcctatgag 420
 ctgactcagg accctgctgt gtctgtggcc ttgggacaga cagtcaggat cacatgccaa 480
 ggagacagcc tcagaagcta ttatgcaagc tggtaccggc agaagccagg acaggcccct 540
 gtacttgtca tctatggtaa aaacaaccgg ccctcaggga tcccagaccg attctctggc 600
 tccagctcgg gaaacacagc ttccttgacc atcattgggg ctcaggcgga agacgaggct 660
 gactattact gtcagtcccg ggacagcagt gataaccgtg ttctattcgg cggagggacc 720
 aaggtcaccg tccta 735

<210> 101
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G03 HCDR1

<400> 101

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 102
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> G03 HCDR2

<400> 102
Ile Asn Pro Gly Thr Gly Tyr Ile
1 5

<210> 103
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> G03 HCDR3

<400> 103
Ser Thr Ala Pro Phe Asp Tyr
1 5

<210> 104
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> G03 LCDR1

<400> 104
Gln Asp Ile Lys Ser Tyr
1 5

<210> 105
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> G03 LCDR2

<400> 105
Tyr Ala Thr
1

<210> 106
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> G03 LCDR3

<400> 106
Leu Gln Tyr Asp Glu Ser Pro Tyr Thr
1 5

<210> 107
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> G03 VH

<400> 107
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

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

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

	85	90	95
Ala Ser Ser Thr	Ala Pro Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val		
100	105	110	

Thr Val Ser Ser
115

<210> 108
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G03 VL

<400> 108
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Asp Ile Lys Ser Tyr
20 25 30

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

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

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

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

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

<210> 109
 <211> 238
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> G03 scFv

<400> 109
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

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

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

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

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

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

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

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

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

 Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Asp Ile
 145 150 155 160

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

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

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

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

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

 <210> 110
 <211> 113
 <212> PRT

<213> Artificial Sequence

<220>

<223> mucin 1

<400> 110

Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser
1 5 10 15

Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp
20 25 30

Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly
35 40 45

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

Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln
65 70 75 80

Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile
85 90 95

Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser
100 105 110

Gly

<210> 111

<211> 182

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic_CD4

<400> 111

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

Phe Pro Leu Asn Leu Gly Glu Glu Ser Leu Gln Gly Glu Leu Arg Trp
20 25 30

Lys Ala Glu Lys Ala Pro Ser Ser Gln Ser Trp Ile Thr Phe Ser Leu
35 40 45

Lys Asn Gln Lys Val Ser Val Gln Lys Ser Thr Ser Asn Pro Lys Phe
 50 55 60
 Gln Leu Ser Glu Thr Leu Pro Leu Thr Leu Gln Ile Pro Gln Val Ser
 65 70 75 80
 Leu Gln Phe Ala Gly Ser Gly Asn Leu Thr Leu Thr Leu Asp Arg Gly
 85 90 95
 Ile Leu Tyr Gln Glu Val Asn Leu Val Val Met Lys Val Thr Gln Pro
 100 105 110
 Asp Ser Asn Thr Leu Thr Cys Glu Val Met Gly Pro Thr Ser Pro Lys
 115 120 125
 Met Arg Leu Ile Leu Lys Gln Glu Asn Gln Glu Ala Arg Val Ser Arg
 130 135 140
 Gln Glu Lys Val Ile Gln Val Gln Ala Pro Glu Ala Gly Val Trp Gln
 145 150 155 160
 Cys Leu Leu Ser Glu Gly Glu Glu Val Lys Met Asp Ser Lys Ile Gln
 165 170 175
 Val Leu Ser Lys Gly Leu
 180

<210> 112
 <211> 135
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> hinge domain

<400> 112
 accacgacgc cagcgccgcg accaccaaca ccggcgccca ccatcgcgtc gcagcccctg 60
 tccctgcgcc cagaggcgtg ccggccagcg gcggggggcg cagtgcacac gagggggctg 120
 gacttcgcct gtgat 135

<210> 113
 <211> 81
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD28 transmembrane domain

<400> 113
 ttttgggtgc tgggtggtggt tgggtggagtc ctggcttgct atagcttgct agtaacagtg 60
 gcctttatta ttttctgggt g 81

<210> 114
 <211> 123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD28 costimulatory domain

<400> 114
 aggagtaaga ggagcaggct cctgcacagt gactacatga acatgactcc ccgccgcccc 60
 gggcccaccc gcaagcatta ccagccctat gccccaccac gcgacttcgc agcctatcgc 120
 tcc 123

<210> 115
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> CD3 zeta intracellular signaling domain

<400> 115
 agagtgaagt tcagcaggag cgcagacgcc cccgcgtacc agcagggcca gaaccagctc 60
 tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120
 cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180
 gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240
 cggagggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300
 tacgacgccc ttcacatgca ggccctgccc cctcgc 336