

SEQUENCE LISTING

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 Varas, Laura

<120> ONCOFETAL ANTIGEN BINDING PROTEINS AND RELATED COMPOSITIONS AND METHODS

<130> APVO-057/03WO 327714-2734

<150> US 62/535,017

<151> 2017-07-20

<150> US 62/575,820

<151> 2017-10-23

<150> US 62/648,072

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<160> 181

<170> PatentIn version 3.5

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Gly Phe Thr Phe Ser His Gly Ser

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Gln Ser Ile Ser Ser Tyr
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 gcagactccg tgaagggccg gttcaccatc tcccatgaca attccaagaa cacgctgtat 240
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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

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

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

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

Lys Gly Arg Phe Thr Ile Ser His 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 Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser

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 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggaag cgggacagat ttactctca ccatcagcag tctacaacct 240
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 1 5 10 15

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

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

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

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

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

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

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<210> 18
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Gly Phe Thr Phe Asp Tyr Gly Ser
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<210> 19
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 ccaggggaagg ggctggagtg ggtctcatct atttcttctg gttctggttc tacatactat 180
 gcagactccg tgaagggccg gttcaccatc tcccacgaca attccaagaa cacgctgtat 240
 ctgcaaataga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct 300
 tactacgggtt cttactactc tattgactat tggggccagg gaaccctggg caccgtctcc 360
 tca 363

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<220>
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<400> 20

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 Tyr Gly
20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser His 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 Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcacagtgg ggtcccatca 180
cgtttcagtg gcagtggaag cgggacagat ttcactctca ccatcagcag tctgcaacct 240
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<212> PRT
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<400> 22

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

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

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

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

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

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

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

<210> 23
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<400> 24

Gly Phe Thr Phe Ser Tyr Gly Ser
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<210> 25
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gcagactccg tgaagggccg gttcaccatc tcccatgaca attccaagaa cacgctgtat      240
ctgcaaataga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct      300
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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Tyr Gly
20           25           30

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

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

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

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

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Ala Arg Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile Asp Tyr Trp Gly
100          105          110

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Gln Gly Thr Leu Val Thr Val Ser Ser
115          120

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ccaggggaagg ggctggagtg ggtctcatct atttcttctg gttctgggtc tacatactat 180
gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat 240
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tca 363

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

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<400> 29
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<210> 30
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 <212> PRT
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<400> 30

Gly Phe Thr Phe Ser Ser Tyr Ala
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<210> 31
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<400> 31
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<210> 32
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<400> 32

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<210> 33
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<400> 33
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<210> 34
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<400> 34

Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr
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<210> 35

<211> 27

<212> DNA

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<211> 9

<212> PRT

<213> ARTIFICIAL SEQUENCE

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<400> 36

Gln Gln Thr Tyr Gly Tyr Leu His Thr
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<210> 37

<211> 363

<212> DNA

<213> ARTIFICIAL SEQUENCE

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cctggaaagg gcctggagtg ggtgtccgct atctccggca gcggcggaag cacctactac 180

gctgactccg tcaagggcag gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga atagcctcag ggctgaagac accgctgtgt actactgcgc cagggtactat 300

ggcggctact actccgctg gatggactac tggggacagg gcacactggt gaccgtgtcc 360

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<212> PRT

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

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

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

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

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

Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 39

<211> 321

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - antibody fragment

<400> 39

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ggaaaggctc ccaagctgct gatctacgcc gcttccagcc tccagagcgg cgtgcctagc 180
aggttctccg gctccggaag cggaacagac ttaccctga ccatcagctc cctgcagccc 240
gaggactccg ctacctacta ctgccagcag acctatggct acctgcacac cttcggccag 300
ggcacaaaagc tggagatcaa g 321

<210> 40

<211> 107

<212> PRT
<213> ARTIFICIAL SEQUENCE

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

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

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

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

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

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

<210> 41
<211> 18
<212> DNA
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<400> 41
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18

<210> 42
<211> 6
<212> PRT
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<400> 42

Gln Ser Ile Ser Ser Phe
1 5

<210> 43

<211> 321
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 ggaaaggctc ccaagctgct gatctacgcc gcttccagcc tccagagcgg cgtgcctagc 180
 aggttctccg gctccggaag cggaacagac ttcaccctga ccatcagctc cctgcagccc 240
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

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

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

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

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

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

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

<210> 45
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 <212> DNA
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cctggaaagt gcctggagtg ggtgtccgct atctccggca gcggcggaag cacctactac      180
gctgactccg tcaagggcag gttcaccatc agccgggaca acagcaagaa caccctgtac      240
ctgcagatga atagcctcag ggctgaagac accgctgtgt actactgcgc caggtactat      300
ggcggctact actccgcctg gatggactac tggggacagg gcacactggg gaccgtgtcc      360
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<210> 46

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<212> PRT

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<400> 46

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

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

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

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

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

Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr Trp Gly
          100          105          110

Gln Gly Thr Leu Val Thr Val Ser Ser
          115          120

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<210> 47

<211> 321
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<223> Made in Lab - antibody fragment

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 ggaaaggctc ccaagctgct gatctacgcc gcttccagcc tccagagcgg cgtgcctagc 180
 aggttctccg gctccggaag cggaacagac ttcaccctga ccatcagctc cctgcagccc 240
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 ggcacaaagc tggagatcaa g 321

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<223> Made in Lab - antibody fragment

<400> 48

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

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

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

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

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

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

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

<210> 49
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<223> Made in Lab - antibody fragment

<400> 49

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ggaaaggctc ccaagctgct gatctacgcc gcttccagcc tccagagcgg cgtgcctagc      180
aggttctccg gctccggaag cggaacagac ttcaccctga ccatcagctc cctgcagccc      240
gaggacttcg ctacctacta ctgccagcag acctatggct acctgcacac cttcggctgc      300
ggcacaaagc tggagatcaa g                                          321

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<210> 50

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<213> Artificial Sequence

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<223> Made in Lab - antibody fragment

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Phe
20           25           30

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

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

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

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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr Leu His
85           90           95

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

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<210> 51

<211> 24

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - antibody fragment

<400> 51
ggcttcgact tcgagagcta tgct 24

<210> 52
<211> 8
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> Made in Lab - antibody fragment

<400> 52

Gly Phe Asp Phe Glu Ser Tyr Ala
1 5

<210> 53
<211> 18
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> Made in Lab - antibody fragment

<400> 53
cagtccatca ggagcgcc 18

<210> 54
<211> 6
<212> PRT
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<220>
<223> Made in Lab - antibody fragment

<400> 54

Gln Ser Ile Arg Ser Ala
1 5

<210> 55
<211> 363
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> Made in Lab - antibody fragment

<400> 55
gaagtgcagc tgctggagtc cggaggagga ctggtgcagc ctggcggaag cctgaggctg 60
agctgcgctg cctccggctt cgacttcgag agctatgcta tgagctgggt gaggcaagcc 120
cctggaaagt gcctggagtg ggtgtccgct atctccggca gcggcggaag cacctactac 180
gctgactccg tcaagggcag gttcaccatc agccgggaca acagcaagaa caccctgtac 240
ctgcagatga atagcctcag ggctgaagac accgctgtgt actactgcgc cagggtactat 300

ggcggctact actccgcctg gatggactac tggggacagg gcacactggt gaccgtgtcc 360
agc 363

<210> 56
<211> 121
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> Made in Lab - antibody fragment

<400> 56

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 Asp Phe Glu Ser Tyr
20 25 30

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

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

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

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

Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 57
<211> 321
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> Made in Lab - antibody fragment

<400> 57

gatattcaga tgacacagtc ccctagctcc ctgtccgccca gcgtgggaga tcgggtgacc 60

atcacctgca gggccagcca gtccatcagg agcgccctga actggtacca gcagaagcct 120

ggaaaggctc ccaagctgct gatctacgcc gcttccagcc tccagagcgg cgtgcctagc 180

aggttctccg gctccggaag cggaacagac ttcaccctga ccatcagctc cctgcagccc 240
gaggacttcg ctacctacta ctgccagcag acctatggct acctgcacac cttcggctgc 300
ggcacaaagc tggagatcaa g 321

<210> 58
<211> 107
<212> PRT
<213> ARTIFICIAL SEQUENCE

<220>
<223> Made in Lab - antibody fragment

<400> 58

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr Leu His
85 90 95

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

<210> 59
<211> 24
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> Made in Lab - antibody fragment

<400> 59

ggcttcgact tcgacagcta tgct 24

<210> 60
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Made in Lab - antibody fragment

<400> 60

Gly Phe Asp Phe Asp Ser Tyr Ala
1 5

<210> 61

<211> 24

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - antibody fragment

<400> 61

atctccggca ggggcggaag cacc

24

<210> 62

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - antibody fragment

<400> 62

Ile Ser Gly Arg Gly Gly Ser Thr
1 5

<210> 63

<211> 363

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - antibody fragment

<400> 63

gaagtgcagc tgctggagtc cggaggagga ctggtgcagc ctggcggaag cctgaggctg 60

agctgcgctg cctccggctt cgacttcgac agctatgcta tgagctgggt gaggcaagcc 120

cctggaaagt gcctggagtg ggtgtccgct atctccggca gggcggaag cacctactac 180

gctgactccg tcaagggcag gttcaccatc agccgggaca acagcaagaa caccctgtac 240

ctgcagatga atagcctcag ggctgaagac accgctgtgt actactgcg cagggtactat 300

ggcggctact actccgctg gatggactac tggggacagg gcacactggt gaccgtgtcc 360

agc 363

<210> 64

<211> 121

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - antibody fragment

<400> 64

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 Asp Phe Asp Ser Tyr
20 25 30

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

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

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

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

Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 65

<211> 321

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - antibody fragment

<400> 65

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atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggaag cgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttatta ctgtcaacag acttacgggt acctgcacac ttttggctgt 300
gggaccaggc tggagatcaa a 321

<210> 66

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - antibody fragment

<400> 66

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr Leu His
 85 90 95

Thr Phe Gly Cys Gly Thr Arg Leu Glu Ile Lys
 100 105

<210> 67

<211> 321

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - antibody fragment

<400> 67

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atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

cgtttcagtg gcagtggaag cgggacagat ttactctca ccatcagcag tctgcaacct 240

gaagattttg caacttatta ctgtcaacag acttacggtt acctgcacac ttttggccag 300

gggaccaagc tggagatcaa a 321

<210> 68

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - antibody fragment

<400> 68

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr Leu His
 85 90 95

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

<210> 69

<211> 321

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - antibody fragment

<400> 69

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 atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggaag cgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttatta ctgtcaacag acttacggtt acctgcacac ttttggtgc 300
 gggaccaagc tggagatcaa a 321

<210> 70

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - antibody fragment

<400> 70

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr Leu His
85 90 95

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

<210> 71
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Hinge/Linker sequence

<400> 71

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1 5 10 15

<210> 72
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Hinge/Linker sequence

<400> 72

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Ser
1 5 10 15

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

<220>
<223> Made in Lab - Hinge/Linker sequence

<400> 73

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Cys Ser
1 5 10 15

<210> 74

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Hinge/Linker sequence

<400> 74

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Ser
1 5 10 15

<210> 75

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Hinge/Linker sequence

<400> 75

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Ser
1 5 10 15

<210> 76

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Hinge/Linker sequence

<400> 76

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Ser
1 5 10 15

<210> 77

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Hinge/Linker sequence

<400> 77

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Cys Ser
1 5 10 15

<210> 78
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 78

Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Cys	Pro
1				5					10					15

<210> 79
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 79

Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro
1				5					10					15

<210> 80
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 80

Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Cys	Pro
1				5					10					15

<210> 81
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 81

Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Cys	Pro
1				5					10					15

<210> 82
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 82

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 83

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Hinge/Linker sequence

<400> 83

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Ser Pro Pro Ser Pro
1 5 10 15

<210> 84

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Hinge/Linker sequence

<400> 84

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Ser Pro
1 5 10 15

<210> 85

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Hinge/Linker sequence

<400> 85

Ser Cys Pro Pro Cys Pro
1 5

<210> 86

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Hinge/Linker sequence

<400> 86

Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15

Ser Gly Asn Ser
20

<210> 87
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Hinge/Linker sequence

<400> 87

Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
1 5 10 15

Ser Gly Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
20 25 30

Gly Gly Ser Gly Asn Ser
35

<210> 88
<211> 2
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Hinge/Linker sequence

<400> 88

Asn Ser
1

<210> 89
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Hinge/Linker sequence

<400> 89

Gly Gly Gly Gly Ser Gly Asn Ser
1 5

<210> 90
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Hinge/Linker sequence

<400> 90

Asn Tyr Gly Gly Gly Gly Ser Gly Asn Ser
1 5 10

<210> 91
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Hinge/Linker sequence

<400> 91

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
1 5 10

<210> 92
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Hinge/Linker sequence

<400> 92

Asn Tyr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asn Ser
1 5 10 15

<210> 93
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Hinge/Linker sequence

<400> 93

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Asn Ser

<210> 94
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Hinge/Linker sequence

<400> 94

Gly Cys Pro Pro Cys Pro Asn Ser
1 5

<210> 95
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 95

Gly Gly Gly Gly Ser
 1 5

<210> 96
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 96

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 97
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 97

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

<210> 98
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 98

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 1 5 10 15

Gly Gly Gly Ser
 20

<210> 99

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

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 99

Gln	Arg	His	Asn	Asn	Ser	Ser	Leu	Asn	Thr	Gly	Thr	Gln	Met	Ala	Gly
1				5					10					15	

His	Ser	Pro	Asn	Ser
			20	

<210> 100
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 100

Ser	Ser	Leu	Asn	Thr	Gly	Thr	Gln	Met	Ala	Gly	His	Ser	Pro	Asn	Ser
1				5					10					15	

<210> 101
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 101

Gln	Arg	His	Asn	Asn	Ser	Ser	Leu	Asn	Thr	Gly	Thr	Gln	Met	Ala	Gly
1				5					10					15	

His Ser

<210> 102
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 102

Glu	Val	Gln	Ile	Pro	Leu	Thr	Glu	Ser	Tyr	Ser	Pro	Asn	Ser
1				5					10				

<210> 103
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 103

Asn Ser Leu Ala Asn Gln Glu Val Gln Ile Pro Leu Thr Glu Ser Tyr
 1 5 10 15

Ser Pro Asn Ser
 20

<210> 104
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 104

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

Pro Asn Ser

<210> 105
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 105

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10 15

Pro Gly Ser

<210> 106
 <211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Hinge/Linker sequence

<400> 106

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

Pro Ala Ser

<210> 107
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Hinge/Linker sequence

<400> 107

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

Pro Ser

<210> 108
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Made in Lab - Hinge/Linker sequence

<400> 108

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

Pro Ser Ser

<210> 109
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in Lab - Synthesized scFv sequence

<400> 109
gaggtgcagc tgttggagag cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc 60
tcctgtgcag ccagcggatt caccttttct cacggttcta tgtactgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcatct atttcttctg gttctgggtc tacatactat 180
gcagactccg tgaagggccg gttcaccatc tcccatgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct 300

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tactacggtt cttactactc tattgactat tggggccagg gaaccctggt caccgtctcc      360
tcaggtggag gtggctccgg ggggtggaggt tccggaggag gcggatcagg tggaggcgga      420
agcgacatcc agatgacca gtctccatcc tccctgagcg catctgtagg agaccgcgtc      480
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa      540
ccagggaaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tgggggtccca      600
tcacgtttca gtggcagtgg aagcgggaca gatttcactc tcaccatcag cagtctacaa      660
cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc      720
caggggacca agctggagat caaa                                             744

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<210> 110

<211> 248

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 110

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

```

```

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

```

```

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

```

```

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

```

```

Lys Gly Arg Phe Thr Ile Ser His 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 Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile Asp Tyr Trp Gly
100          105          110

```

```

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

```

```

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

```

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

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

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

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

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

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

Gln Gly Thr Lys Leu Glu Ile Lys
245

<210> 111
<211> 744
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in Lab - Synthesized scFv sequence

<400> 111
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tcctgtgcag ccagcggatt cacctttgat tacggttcta tgtactgggt ccgccaggct 120
ccaggggaagg ggctggagtg ggtctcatct atttcttctg gttctggttc tacatactat 180
gcagactccg tgaagggccg gttcaccatc tcccacgaca attccaagaa cacgctgtat 240
ctgcaaataga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct 300
tactacggtt cttactactc tattgactat tggggccagg gaaccctggt caccgtctcc 360
tcaggtggag gtggctccgg ggggtggagg tccggaggag gcggatcagg tggaggcgga 420
agcgacatcc agatgacca gtctccatcc tccctgagcg catctgtagg agaccgcgtc 480
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa 540
ccagggaaag cccctaagct cctgatctat gctgcatcca gtttgacag tgggggtccca 600
tcacgtttca gtggcagtgg aagcgggaca gatttcactc tcaccatcag cagtctgcaa 660
cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc 720
caggggacca agctggagat caaa 744

<210> 112
 <211> 248
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Synthesized scFv sequence

<400> 112

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 Tyr Gly
 20 25 30

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

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

Lys Gly Arg Phe Thr Ile Ser His 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 Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile Asp Tyr Trp Gly
 100 105 110

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

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

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

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

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

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

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

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

Gln Gly Thr Lys Leu Glu Ile Lys
 245

<210> 113
 <211> 744
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Synthesized scFv sequence

<400> 113
 gaggtgcagc tgttgagagc cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc 60
 tcctgtgcag ccagcggatt caccttttct tacggttcta tgtactgggt ccgccaggct 120
 ccaggggaagg ggctggagtg ggtctcatct atttcttctg gttctgggtc tacatactat 180
 gcagactccg tgaagggccg gttcaccatc tcccatgaca attccaagaa cacgctgtat 240
 ctgcaaatac acagcctgcg tgccgaggac acggtgtat attattgtgc gcgctcttct 300
 tactacggtt cttactactc tattgactat tggggccagg gaaccctggc caccgtctcc 360
 tcaggtggag gtggctccgg gggaggaggc tccggaggag gcggatcagg tggaggcgga 420
 agcgacatcc agatgacca gtctccatcc tccctgagcg catctgtagg agaccgcgtc 480
 accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa 540
 ccagggaaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tgggggtccca 600
 tcacgtttca gtggcagtgg aagcgggaca gatttactc tcaccatcag cagtctacaa 660
 cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc 720
 caggggacca agctggagat caaa 744

<210> 114
 <211> 248
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - Synthesized scFv sequence

<400> 114

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

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

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

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

Lys Gly Arg Phe Thr Ile Ser His 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 Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile Asp Tyr Trp Gly
100 105 110

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

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

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

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

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

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

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

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

Gln Gly Thr Lys Leu Glu Ile Lys
245

<210> 115

<211> 744

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 115

```

gaggtgcagc tgttgagag cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc      60
tcctgtgcag ccagcggatt caccttttct tacggttcta tgtactgggt ccgccaggct      120
ccaggaagg ggctggagtg ggtctcatct atttcttctg gttctgggtc tacatactat      180
gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct      300
tactacggtt cttactactc tattgactat tggggccagg gaaccctggg caccgtctcc      360
tcaggcggcg gcggcagcgg cggcggcggc agcggcggcg gaggtccgg cggcggcggc      420
agcgacatcc agatgacca gtctccatcc tccctgagcg catctgtagg agaccgcgtc      480
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa      540
ccagggaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tgggggtccca      600
tcacgtttca gtggcagtgg aagcgggaca gatttcactc tcaccatcag cagtctgcaa      660
cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc      720
caggggacca agctggagat caaa                                         744

```

<210> 116

<211> 248

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 116

```

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

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

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

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

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

```

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

Ala Arg Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile Asp Tyr Trp Gly
100 105 110

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

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

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

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

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

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

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

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

Gln Gly Thr Lys Leu Glu Ile Lys
245

<210> 117

<211> 744

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 117

gaagtgcagc tgctggagtc cggaggagga ctggtgcagc ctggcggaag cctgaggctg	60
agctgcgctg cctccggctt cacattcagc agctatgcta tgagctgggt gaggcaagcc	120
cctggaaagg gcctggagtg ggtgtccgct atctccggca gcggcggaag cacctactac	180
gctgactccg tcaagggcag gttcaccatc agccgggaca acagcaagaa caccctgtac	240
ctgcagatga atagcctcag ggctgaagac accgctgtgt actactgcgc caggtactat	300

```

ggcgggtact actccgcctg gatggactac tggggacagg gcacactggt gaccgtgtcc      360
agcggcgagg gcggtctccg aggcgggtggc tccggaggag gcggaagcgg aggaggaggc      420
tccgatattc agatgacaca gtcccctagc tccctgtccg ccagcgtggg agatcgggtg      480
accatcacct gcagggccag ccagtccatc tccagctatt taaactggta ccagcagaag      540
cctggaaagg ctcccaagct gctgatctac gccgcttcca gcctccagag cggcgtgcct      600
agcaggttct ccggctccg aagcggaaca gacttcaccc tgaccatcag ctccctgcag      660
cccgaggact ccgtaccta ctactgccag cagacctatg gctacctgca caccttcggc      720
cagggcacia agctggagat caag                                             744

```

```

<210> 118
<211> 248
<212> PRT
<213> ARTIFICIAL SEQUENCE

```

```

<220>
<223> Made in Lab - Synthesized scFv sequence

```

```

<400> 118

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr Trp Gly
100          105          110

```

```

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

```

```

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

```

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

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

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

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

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

Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr Leu His Thr Phe Gly
225 230 235 240

Gln Gly Thr Lys Leu Glu Ile Lys
245

<210> 119

<211> 744

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 119

```

gaagtgcagc tgctggagtc cggaggagga ctggtgcagc ctggcggaag cctgaggctg      60
agctgcgctg cctccggctt cacattcagc agctatgcta tgagctgggt gaggcaagcc      120
cctggaaagg gcctggagtg ggtgtccgct atctccggca gcggcggaag cacctactac      180
gctgactccg tcaagggcag gtccaccatc agccgggaca acagcaagaa caccctgtac      240
ctgcagatga atagcctcag ggctgaagac accgctgtgt actactgcgc cagggtactat      300
ggcggctact actccgcctg gatggactac tggggacagg gcacactggg gaccgtgtcc      360
agcggcgag gcggtccgg aggcggtggc tccggaggag gcggaagcgg aggaggaggc      420
tccgatattc agatgacaca gtcccctagc tccctgtccg ccagcgtggg agatcgggtg      480
accatcacct gcagggccag ccagtcctatc tccagcttct taaactggta ccagcagaag      540
cctggaaagg ctcccaagct gctgatctac gccgcttcca gcctccagag cggcgtgcct      600
agcaggttct ccggctccgg aagcggaaca gacttcaccc tgaccatcag ctccctgcag      660
cccgaggact ccgtaccta ctactgccag cagacctatg gctacctgca caccttcggc      720
cagggcacia agctggagat caag                                         744

```

<210> 120
 <211> 248
 <212> PRT
 <213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 120

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

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

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

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

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

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

Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr Trp Gly
 100 105 110

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

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

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

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Phe Leu Asn Trp
 165 170 175

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

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

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

Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr Leu His Thr Phe Gly
 225 230 235 240

Gln Gly Thr Lys Leu Glu Ile Lys
 245

<210> 121
 <211> 744
 <212> DNA
 <213> ARTIFICIAL SEQUENCE

<220>
 <223> Made in Lab - Synthesized scFv sequence

<400> 121
 gaagtgcagc tgctggagtc cggaggagga ctggtgcagc ctggcggaag cctgaggctg 60
 agctgcgctg cctccggctt cacattcagc agctatgcta tgagctgggt gaggcaagcc 120
 cctggaaagt gcctggagtg ggtgtccgct atctccggca gcggcggaag cacctactac 180
 gctgactccg tcaagggcag gttcaccatc agccgggaca acagcaagaa caccctgtac 240
 ctgcagatga atagcctcag ggctgaagac accgctgtgt actactgcgc caggtactat 300
 ggcggctact actccgcctg gatggactac tggggacagg gcacactggt gaccgtgtcc 360
 agcggcgag gcggctccgg aggcggtggc tccggaggag gcggaagcgg aggaggaggc 420
 tccgatattc agatgacaca gtcccctagc tccctgtccg ccagcgtggg agatcgggtg 480
 accatcacct gcagggccag ccagtccatc tccagcttct taaactggta ccagcagaag 540
 cctggaaagg ctcccaagct gctgatctac gccgcttcca gcctccagag cggcgtgcct 600
 agcaggttct ccggtccgg aagcgggaaca gacttcaccc tgaccatcag ctccctgcag 660
 cccgaggact ccgctaccta ctactgccag cagacctatg gctacctgca caccttcggc 720
 tgcggcacia agctggagat caag 744

<210> 122
 <211> 248
 <212> PRT
 <213> ARTIFICIAL SEQUENCE

<220>
 <223> Made in Lab - Synthesized scFv sequence

<400> 122

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

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

20

25

30

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

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

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

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

Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr Trp Gly
 100 105 110

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

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

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

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Phe Leu Asn Trp
 165 170 175

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

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

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

Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr Leu His Thr Phe Gly
 225 230 235 240

Cys Gly Thr Lys Leu Glu Ile Lys
 245

<210> 123

<211> 744

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 123

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gaagtgcagc tgctggagtc cggaggagga ctggtgcagc ctggcggaag cctgaggctg      60
agctgcgctg cctccggctt cacattcagc agctatgcta tgagctgggt gaggcaagcc      120
cctggaaagt gcctggagtg ggtgtccgct atctccggca gcggcggaag cacctactac      180
gctgactccg tcaagggcag gttcaccatc agccgggaca acagcaagaa caccctgtac      240
ctgcagatga atagcctcag ggctgaagac accgctgtgt actactgcgc caggtactat      300
ggcggctact actccgcctg gatggactac tggggacagg gcacactggg gaccgtgtcc      360
agcggcgag gcggtccgg aggcggtggc tccggaggag gcggaagcgg aggaggaggc      420
tccgatattc agatgacaca gtcccctagc tccctgtccg ccagcgtggg agatcgggtg      480
accatcacct gcagggccag ccagtccatc tccagcttct taaactggta ccagcagaag      540
cctggaaagg ctccaagct gctgatctac gccgcttcca gcctccagag cggcgtgcct      600
agcaggttct ccggctccgg aagcggaaca gacttcaccc tgaccatcag ctccctgcag      660
cccgaggact tcgctaccta ctactgccag cagacctatg gctacctgca caccttcggc      720
tgcggcacaa agctggagat caag                                             744

```

<210> 124

<211> 248

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 124

```

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

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

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

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

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

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

```

85

90

95

Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr Trp Gly
100 105 110

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

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

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

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Phe Leu Asn Trp
165 170 175

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

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

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

Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr Leu His Thr Phe Gly
225 230 235 240

Cys Gly Thr Lys Leu Glu Ile Lys
245

<210> 125

<211> 744

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 125

gaagtgcagc tgctggagtc cggaggagga ctggtgcagc ctggcggaag cctgaggctg	60
agctgcgctg cctccggctt cgacttcgag agctatgcta tgagctgggt gaggcaagcc	120
cctggaaagt gcctggagtg ggtgtccgct atctccggca gcggcggaag cacctactac	180
gctgactccg tcaagggcag gttcaccatc agccgggaca acagcaagaa caccctgtac	240
ctgcagatga atagcctcag ggctgaagac accgctgtgt actactgcgc cagggtactat	300
ggcggctact actccgcctg gatggactac tggggacagg gcacactggg gaccgtgtcc	360

```

agcggcgagg gcggtccgg aggcgggtggc tccggaggag gcggaagcgg aggaggaggc      420
tccgatattc agatgacaca gtcccctagc tccctgtccg ccagcgtggg agatcgggtg      480
accatcacct gcagggccag ccagtccatc aggagcgccc tgaactggta ccagcagaag      540
cctggaaagg ctcccaagct gctgatctac gccgcttcca gcctccagag cggcgtgcct      600
agcaggttct ccggctccgg aagcggaaca gacttcaccc tgaccatcag ctccctgcag      660
cccgaggact tcgctaccta ctactgccag cagacctatg gctacctgca caccttcggc      720
tgcggcacaa agctggagat caag                                             744

```

<210> 126

<211> 248

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 126

```

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 Asp Phe Glu Ser Tyr
          20              25              30

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr Trp Gly
          100              105              110

```

```

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

```

```

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

```

```

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val

```

<400>	127						
gaagtgcagc	tgctggagtc	cggaggagga	ctggtgcagc	ctggcggaaag	cctgaggctg		60
agctgcgctg	cctccggctt	cgacttcgac	agctatgcta	tgagctgggt	gaggcaagcc		120
cctggaaagt	gcctggagtg	ggtgtccgct	atctccggca	ggggcggaaag	cacctactac		180
gctgactccg	tcaagggcag	gttcaccatc	agccgggaca	acagcaagaa	caccctgtac		240
ctgcagatga	atagcctcag	ggctgaagac	accgctgtgt	actactgcg	caggtactat		300
ggcggctact	actccgcctg	gatggactac	tggggacagg	gcacactggt	gaccgtgtcc		360
agcggcggag	gcggctccgg	aggcgggtgg	tccggaggag	gcggaagcgg	aggaggaggc		420
tccgatattc	agatgacaca	gtcccctagc	tccctgtccg	ccagcgtggg	agatcgggtg		480
accatcacct	gcagggccag	ccagtcctac	aggagcgccc	tgaactggta	ccagcagaag		540
cctggaaagg	ctcccaagct	gctgatctac	gccgcttcca	gcctccagag	cggcgtgcct		600
agcaggttct	ccggctccgg	aagcgggaaca	gacttcaccc	tgaccatcag	ctccctgcag		660
cccgaggact	tcgctaccta	ctactgccag	cagacctatg	gctacctgca	caccttcggc		720
tgcggcacaa	agctggaagt	caag					744

<210> 128
 <211> 248
 <212> PRT
 <213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 128

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 Asp Phe Asp Ser Tyr
 20 25 30

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

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

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

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

Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr Trp Gly
 100 105 110

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

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

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

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

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

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

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

210

215

220

Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr Leu His Thr Phe Gly
 225 230 235 240

Cys Gly Thr Lys Leu Glu Ile Lys
 245

<210> 129

<211> 744

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 129

gaggtgcagc tgttggagag cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc 60
 tcctgtgcag ccagcggatt caccttttagc agctatgccca tgagctgggt ccgccaggct 120
 ccagggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactat 180
 gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat 240
 ctgcaaataga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctactac 300
 ggtgggttact actctgcttg gatggactat tggggccagg gaaccctggc caccgtctcc 360
 tcaggcgggtg gaggcagcgg tgggggtggg tctggaggcg gtggcagtg cggcggaggc 420
 tctgacatcc agatgacca gtctccatcc tccctgagcg catctgtagg agaccgcgtc 480
 accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa 540
 ccagggaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tggggtccca 600
 tcacgtttca gtggcagtg aagcgggaca gatttcactc tcaccatcag cagtctgcaa 660
 cctgaagatt ttgcaactta ttactgtcaa cagacttacg gttacctgca cacttttggc 720
 caggggacca agctggagat caaa 744

<210> 130

<211> 248

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 130

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

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

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

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

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

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

Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr Trp Gly
100 105 110

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

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

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

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

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

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

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

Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr Leu His Thr Phe Gly
225 230 235 240

Gln Gly Thr Lys Leu Glu Ile Lys
245

<210> 131

<211> 744

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 131

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gaggtgcagc tgttgagag cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc      60
tcctgtgcag ccagcggatt caccttttagc agctatgcc a tgagctgggt ccgccaggct      120
ccaggggaagt gcctggagtg ggtctcagct attagtggta gtggtggtag cacatactat      180
gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctactac      300
ggcgtgttact actctgcttg gatggactat tggggccagg gaaccctggc caccgtctcc      360
tcaggcgggtg gaggcagcgg tgggggtggg tctggaggcg gtggcagtg cggcggaggc      420
tctgacatcc agatgacca gtctccatcc tccctgagcg catctgtagg agaccgcgtc      480
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa      540
ccagggaaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tgggggtccca      600
tcacgtttca gtggcagtg aagcgggaca gatttcactc tcaccatcag cagtctgcaa      660
cctgaagatt ttgcaactta ttactgtcaa cagacttacg gttacctgca cacttttggc      720
tgcgggacca agctggagat caaa                                           744

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<210> 132

<211> 248

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 132

```

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

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

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

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

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

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

```

Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr Trp Gly
100 105 110

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

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

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

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

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

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

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

Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr Leu His Thr Phe Gly
225 230 235 240

Cys Gly Thr Lys Leu Glu Ile Lys
245

<210> 133
<211> 744
<212> DNA
<213> ARTIFICIAL SEQUENCE

<220>
<223> Made in Lab - Synthesized scFv sequence

<400> 133
gacatccaga tgaccagtc tccatcctcc ctgagcgcac ctgtaggaga ccgcgtcacc 60
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtggaag cgggacagat ttactctca ccatcagcag tctgcaacct 240
gaagattttg caacttatta ctgtcaacag acttacggtt acctgcacac ttttggtgc 300
gggaccaagc tggagatcaa aggcggtgga ggcagcgggtg ggggtgggtc tggaggcgg 360

```

ggcagtggcg gcgaggctc tgaggtgcag ctgttgaga gcgggggagg cttggtacag      420
cctgggggggt ccctgcgcct ctctgtgca gccagcggat tcacctttag cagctatgcc      480
atgagctggg tccgccaggc tccaggaag tgcctggagt gggctctcagc tattagtgg      540
agtggtggtg gcacatacta tgcagactcc gtgaagggcc gggtcaccat ctcccgtgac      600
aattccaaga acacgtgtg tctgcaaag aacagcctgc gtgccgagga cacggctgta      660
tattattgtg cgcgctacta cggtggttac tactctgctt ggatggacta ttggggccag      720
ggaaccctgg tcaccgtctc ctca                                           744

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<210> 134

<211> 248

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> Made in Lab - Synthesized scFv sequence

<400> 134

```

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

```

```

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

```

```

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

```

```

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

```

```

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

```

```

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr Leu His
          85          90          95

```

```

Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
          100          105          110

```

```

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

```

```

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

```

```

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala
145          150          155          160

```

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Ser
 165 170 175

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

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

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 210 215 220

Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr Trp Gly Gln
 225 230 235 240

Gly Thr Leu Val Thr Val Ser Ser
 245

<210> 135

<211> 2304

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polynucleotide construct

<400> 135

atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt	60
gaggtgcagc tgttgagag cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc	120
tcctgtgcag ccagcggatt caccttttct cacggttcta tgtactgggt ccgccaggct	180
ccaggggaagg ggctggagt ggtctcatct atttcttctg gttctggttc tacatactat	240
gcagactccg tgaagggccg gttcaccatc tcccatgaca attccaagaa cacgctgtat	300
ctgcaaatga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct	360
tactacggtt cttactactc tattgactat tggggccagg gaaccctggt caccgtctcc	420
tcaggtggag gtggctccgg ggggtggagg tccggaggag gcggatcagg tggaggcgga	480
agcgacatcc agatgaccca gtctccatcc tccctgagcg catctgtagg agaccgcgtc	540
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa	600
ccagggaaag ccctaagct cctgatctat gctgcatcca gtttgcaaag tgggggtcca	660
tcacgtttca gtggcagtgg aagcgggaca gatttcactc tcaccatcag cagtctacaa	720
cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc	780
caggggacca agctggagat caaatcgagt gagcccaaat cttctgacaa aactcacaca	840

```

tgcccaccgt gccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttcccccca 900
aaaccaagg acaccctcat gatctcccg acccctgagg tcacatgcgt ggtggtggac 960
gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020
aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080
ctcacgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140
aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa 1200
ccacaggtgt acaccctgcc cccatcccg gatgagctga ccaagaacca ggtcagcctg 1260
acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg 1320
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctcttcttc 1380
ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440
tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg 1500
ggttccggag gtggcggttc gggaggtggc gggtcaggag gtgggggatc cccttcagaa 1560
gtgcagctgc tggagtccgg aggaggactg gtgcagcctg gcggaagcct gaggctgagc 1620
tgcgtgcct ccggcttcac attcagcagc tatgctatga gctgggtgag gcaagcccct 1680
ggaaagggcc tggagtgggt gtccgctatc tccggcagcg gcggaagcac ctactacgct 1740
gactccgtca agggcaggtt caccatcagc cgggacaaca gcaagaacac cctgtacctg 1800
cagatgaata gcctcagggc tgaagacacc gctgtgtact actgcgccag gtactatggc 1860
ggctactact ccgcctggat ggactactgg ggacagggca cactggtgac cgtgtccagc 1920
ggcggaggcg gctccggagg cgggtggctcc ggaggaggcg gaagcggagg aggaggctcc 1980
gatattcaga tgacacagtc ccctagctcc ctgtccgcca gcgtgggaga tcgggtgacc 2040
atcacctgca gggccagcca gtccatctcc agctatttaa actggtacca gcagaagcct 2100
ggaaaggctc ccaagctgct gatctacgcc gcttcagacc tccagagcgg cgtgcctagc 2160
aggttctccg gctccggaag cggaacagac ttcaccctga ccatcagctc cctgcagccc 2220
gaggactccg ctacctacta ctgccagcag acctatggct acctgcacac cttcggccag 2280
ggcaciaaagc tggagatcaa gcgc 2304

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<210> 136

<211> 768

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polypeptide construct

<400> 136

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
1 5 10 15

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

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
 35 40 45

Phe Ser His Gly Ser Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly
 50 55 60

Leu Glu Trp Val Ser Ser Ile Ser Ser Gly Ser Gly Ser Thr Tyr Tyr
 65 70 75 80

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser His Asp Asn Ser Lys
 85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 100 105 110

Val Tyr Tyr Cys Ala Arg Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile
 115 120 125

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 145 150 155 160

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 165 170 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
 180 185 190

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

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

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asp Asn Leu
 245 250 255

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

260

265

270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 275 280 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 290 295 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 305 310 315 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 325 330 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 340 345 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 355 360 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
 370 375 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 385 390 395 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 405 410 415

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 420 425 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 435 440 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 450 455 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 465 470 475 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 485 490 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 500 505 510

Gly Gly Gly Gly Ser Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly
 515 520 525

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 530 535 540

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro
 545 550 555 560

Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser
 565 570 575

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 580 585 590

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
 595 600 605

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser
 610 615 620

Ala Trp Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 625 630 635 640

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 645 650 655

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 660 665 670

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
 675 680 685

Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 690 695 700

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
 705 710 715 720

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
 725 730 735

Ser Leu Gln Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr
 740 745 750

Gly Tyr Leu His Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 755 760 765

<210> 137
 <211> 2304
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polynucleotide construct

<400> 137

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atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt      60
gaggtgcagc tggtggagag cgggggagggc ttggtacagc ctgggggggtc cctgcgcctc      120
tcctgtgcag ccagcggatt caccttttct cacggttcta tgtactgggt ccgccaggct      180
ccaggggaagg ggctggagtg ggtctcatct atttcttctg gttctgggtc tacatactat      240
gcagactccg tgaagggccg gttcaccatc tcccatgaca attccaagaa cacgctgtat      300
ctgcaaatga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct      360
tactacgggt cttactactc tattgactat tggggccagg gaaccctggg caccgtctcc      420
tcaggtggag gtggctccgg ggggtggaggt tccggaggag gcggatcagg tggaggcgga      480
agcgacatcc agatgaccca gtctccatcc tccctgagcg catctgtagg agaccgcgtc      540
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa      600
ccagggaaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tgggggtccca      660
tcacgtttca gtggcagtgg aagcgggaca gatttcactc tcaccatcag cagtctacaa      720
cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc      780
caggggacca agctggagat caaatcgagt gagcccaaat cttctgacaa aactcacaca      840
tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttcccccca      900
aaaccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac      960
gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat     1020
aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc     1080
ctcacgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac     1140
aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa     1200
ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg     1260
acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg     1320
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc     1380
ctctacagca agctcacctg ggacaagagc aggtggcagc aggggaacgt cttctcatgc     1440
tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg     1500
ggttccggag gtggcggttc gggaggtggc gggtcaggag gtgggggatc cccttcagaa     1560
gtgcagctgc tggagtccgg aggaggactg gtgcagcctg gcggaagcct gaggctgagc     1620

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```

tgcgctgcct cgggcttcac attcagcagc tatgctatga gctgggtgag gcaagcccct 1680
ggaaagggcc tggagtgggt gtccgctatc tccggcagcg gcggaagcac ctactacgct 1740
gactccgtca agggcaggtt caccatcagc cgggacaaca gcaagaacac cctgtacctg 1800
cagatgaata gcctcagggc tgaagacacc gctgtgtact actgcgccag gtactatggc 1860
ggctactact ccgcctggat ggactactgg ggacagggca cactgggtgac cgtgtccagc 1920
ggcggaggcg gctccggagg cggtaggctcc ggaggaggcg gaagcggagg aggaggctcc 1980
gatattcaga tgacacagtc ccctagctcc ctgtccgccg gcgtgggaga tcgggtgacc 2040
atcacctgca gggccagcca gtccatctcc agcttcttaa actggtacca gcagaagcct 2100
ggaaaggctc ccaagctgct gatctacgcc gcttccagcc tccagagcgg cgtgcctagc 2160
aggttctccg gctccggaag cggaacagac ttaccctga ccatcagctc cctgcagccc 2220
gaggactccg ctacctacta ctgccagcag acctatggct acctgcacac cttcggccag 2280
ggcacaaaagc tggagatcaa gcgc 2304

```

<210> 138

<211> 768

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polypeptide construct

<400> 138

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Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
1           5           10           15

```

```

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

```

```

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
35           40           45

```

```

Phe Ser His Gly Ser Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly
50           55           60

```

```

Leu Glu Trp Val Ser Ser Ile Ser Ser Gly Ser Gly Ser Thr Tyr Tyr
65           70           75           80

```

```

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser His Asp Asn Ser Lys
85           90           95

```

```

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
100          105          110

```

Val	Tyr	Tyr	Cys	Ala	Arg	Ser	Ser	Tyr	Tyr	Gly	Ser	Tyr	Tyr	Ser	Ile
			115				120					125			
Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly
	130					135					140				
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
145					150					155					160
Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val
				165					170					175	
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser
			180					185					190		
Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu
		195					200					205			
Ile	Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser
	210					215					220				
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln
225					230					235					240
Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Tyr	Asp	Asn	Leu
				245					250					255	
Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Ser	Ser	Glu	Pro
			260					265						270	
Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu
		275					280					285			
Ala	Ala	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp
	290					295					300				
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
305					310					315					320
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly
				325					330					335	
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn
			340					345					350		
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp
		355					360					365			

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
 370 375 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 385 390 395 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 405 410 415

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 420 425 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 435 440 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 450 455 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 465 470 475 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 485 490 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 500 505 510

Gly Gly Gly Gly Ser Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly
 515 520 525

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 530 535 540

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro
 545 550 555 560

Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser
 565 570 575

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 580 585 590

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
 595 600 605

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser

610	615	620	
Ala Trp Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser			
625	630	635	640
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly			
	645	650	655
Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser			
	660	665	670
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser			
	675	680	685
Ile Ser Ser Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro			
	690	695	700
Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser			
	705	710	715
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser			
	725	730	735
Ser Leu Gln Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr			
	740	745	750
Gly Tyr Leu His Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg			
	755	760	765
<210> 139			
<211> 2304			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> Made in Lab - anti-5T4 x anti-4-1BB polynucleotide construct			
<400> 139			
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt			60
gaggtgcagc tgttgagag cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc			120
tcctgtgcag ccagcggatt caccttttct cacggttcta tgtactgggt ccgccaggct			180
ccaggggaagg ggctggagt ggtctcatct atttcttctg gttctggttc tacatactat			240
gcagactccg tgaagggccg gttcaccatc tcccatgaca attccaagaa cacgctgtat			300
ctgcaaatga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct			360
tactacgggt cttactactc tattgactat tggggccagg gaaccctggt caccgtctcc			420
tcaggtggag gtggctccgg ggggtggaggt tccggaggag gcggatcagg tggaggcgga			480

agcgacatcc agatgaccca gtctccatcc tccctgagcg catctgtagg agaccgcgtc	540
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa	600
ccagggaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tggggtccca	660
tcacgtttca gtggcagtgg aagcgggaca gatttcactc tcaccatcag cagtctacaa	720
cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc	780
caggggacca agctggagat caaatcgagt gagcccaaat cttctgacaa aactcacaca	840
tgccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttcccccca	900
aaaccaagg acaccctcat gatctcccg acccctgagg tcacatgcgt ggtggtggac	960
gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat	1020
aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc	1080
ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac	1140
aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa	1200
ccacaggtgt acaccctgcc cccatcccg gatgagctga ccaagaacca ggtcagcctg	1260
acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg	1320
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctctctcttc	1380
ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc	1440
tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg	1500
ggttccggag gtggcggttc gggaggtggc gggtcaggag gtgggggatc cccttcagaa	1560
gtgcagctgc tggagtccgg aggaggactg gtgcagcctg gcggaagcct gaggctgagc	1620
tgcgtgcct ccggcttcac attcagcagc tatgctatga gctgggtgag gcaagcccct	1680
ggaaagtgcc tggagtgggt gtccgctatc tccggcagcg gcggaagcac ctactacgct	1740
gactccgtca agggcaggtt caccatcagc cgggacaaca gcaagaacac cctgtacctg	1800
cagatgaata gcctcagggc tgaagacacc gctgtgtact actgcgccag gtactatggc	1860
ggctactact ccgcctggat ggactactgg ggacagggca cactggtgac cgtgtccagc	1920
ggcggaggcg gctccggagg cggaggctcc ggaggaggcg gaagcggagg aggaggctcc	1980
gatattcaga tgacacagtc ccctagctcc ctgtccgcca gcgtgggaga tcgggtgacc	2040
atcacctgca gggccagcca gtccatctcc agcttcttaa actggtacca gcagaagcct	2100
ggaaaggctc ccaagctgct gatctacgcc gcttccagcc tccagagcgg cgtgcctagc	2160
aggttctccg gctccggaag cggaacagac ttcacctga ccatcagctc cctgcagccc	2220
gaggactccg ctacctacta ctgccagcag acctatggct acctgcacac cttcggtgc	2280
ggcacaaagc tggagatcaa gcgc	2304

<210> 140
 <211> 768
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polypeptide construct

<400> 140

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
 1 5 10 15

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

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
 35 40 45

Phe Ser His Gly Ser Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly
 50 55 60

Leu Glu Trp Val Ser Ser Ile Ser Ser Gly Ser Gly Ser Thr Tyr Tyr
 65 70 75 80

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser His Asp Asn Ser Lys
 85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 100 105 110

Val Tyr Tyr Cys Ala Arg Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile
 115 120 125

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 145 150 155 160

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 165 170 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
 180 185 190

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

Ile	Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	210	215	220	
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	225	230	235	240
Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Tyr	Asp	Asn	Leu	245	250	255	
Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Ser	Ser	Glu	Pro	260	265	270	
Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	275	280	285	
Ala	Ala	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	290	295	300	
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	305	310	315	320
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	325	330	335	
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	340	345	350	
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	355	360	365	
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Ala	Val	Ser	Asn	Lys	Ala	Leu	Pro	370	375	380	
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	385	390	395	400
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	405	410	415	
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	420	425	430	
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	435	440	445	
Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	450	455	460	

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 465 470 475 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 485 490 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 500 505 510

Gly Gly Gly Gly Ser Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly
 515 520 525

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 530 535 540

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro
 545 550 555 560

Gly Lys Cys Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser
 565 570 575

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 580 585 590

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
 595 600 605

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser
 610 615 620

Ala Trp Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 625 630 635 640

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 645 650 655

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
 660 665 670

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
 675 680 685

Ile Ser Ser Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
 690 695 700

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
 705 710 715 720

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
725 730 735

Ser Leu Gln Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr
740 745 750

Gly Tyr Leu His Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys Arg
755 760 765

<210> 141

<211> 2304

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polynucleotide construct

<400> 141

atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt	60
gaggtgcagc tgttggagag cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc	120
tcctgtgcag ccagcggatt cacctttgat tacggttcta tgtactgggt ccgccaggct	180
ccaggggaagg ggctggagtg ggtctcatct atttcttctg gttctggttc tacatactat	240
gcagactccg tgaagggccg gttcaccatc tcccacgaca attccaagaa cacgctgtat	300
ctgcaaatga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct	360
tactacggtt cttactactc tattgactat tggggccagg gaaccctggg caccgtctcc	420
tcaggtggag gtggctccgg ggggtggaggt tccggaggag gcggatcagg tggaggcgga	480
agcgacatcc agatgaccca gtctccatcc tccctgagcg catctgtagg agaccgcgtc	540
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa	600
ccagggaaag cccctaagct cctgatctat gctgcatcca gtttgacag tgggggtcca	660
tcacgtttca gtggcagtg aagcgggaca gatttcactc tcaccatcag cagtctgcaa	720
cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc	780
caggggacca agctggagat caaatcctcg gagcccaaat cttctgacaa aactcacaca	840
tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttcccccca	900
aaaccaagg acaccctcat gatctcccg acccctgagg tcacatgcgt ggtggtggac	960
gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat	1020
aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc	1080
ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac	1140
aaagccctcc cagcccccat cgagaaaacc atctccaaag ccaaagggca gccccgagaa	1200

```

ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg      1260
acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg      1320
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctcccttcttc      1380
ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc      1440
tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg      1500
ggttccggag gtggcggttc gggaggtggc gggtcaggag gtgggggatc cccttcagaa      1560
gtgcagctgc tggagtccgg aggaggactg gtgcagcctg gcggaagcct gaggctgagc      1620
tgcgctgcct ccggcttcac attcagcagc tatgctatga gctgggtgag gcaagcccct      1680
ggaaagtgcc tggagtgggt gtccgctatc tccggcagcg gcggaagcac ctactacgct      1740
gactccgtca agggcaggtt caccatcagc cgggacaaca gcaagaacac cctgtacctg      1800
cagatgaata gcctcagggc tgaagacacc gctgtgtact actgcgccag gtactatggc      1860
ggctactact ccgcctggat ggactactgg ggacagggca cactggtgac cgtgtccagc      1920
ggcggaggcg gctccggagg cggtggtcc ggaggaggcg gaagcggagg aggaggctcc      1980
gatattcaga tgacacagtc ccctagctcc ctgtccgcc gcgtagggaga tcgggtgacc      2040
atcacctgca gggccagcca gtccatctcc agcttcttaa actggtacca gcagaagcct      2100
ggaaaggctc ccaagctgct gatctacgcc gcttccagcc tccagagcgg cgtgcctagc      2160
aggttctccg gctccggaag cggaacagac ttcaccctga ccatcagctc cctgcagccc      2220
gaggacttcg ctacctacta ctgccagcag acctatggct acctgcacac cttcgggtgc      2280
ggcacaaagc tggagatcaa gaggc      2304

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<210> 142

<211> 768

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polypeptide construct

<400> 142

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Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1           5           10           15

```

```

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

```

```

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
35           40           45

```

```

Phe Asp Tyr Gly Ser Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly
50           55           60

```

Leu Glu Trp Val Ser Ser Ile Ser Ser Gly Ser Gly Ser Thr Tyr Tyr
65 70 75 80

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser His Asp Asn Ser Lys
85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
100 105 110

Val Tyr Tyr Cys Ala Arg Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile
115 120 125

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
165 170 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
180 185 190

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

Ile Tyr Ala Ala Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser
210 215 220

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asp Asn Leu
245 250 255

Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ser Ser Glu Pro
260 265 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
275 280 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
290 295 300

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

305		310		315		320
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly						
		325		330		335
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn						
		340		345		350
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp						
		355		360		365
Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro						
		370		375		380
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu						
		385		390		400
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn						
		405		410		415
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile						
		420		425		430
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr						
		435		440		445
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys						
		450		455		460
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys						
		465		470		475
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu						
		485		490		495
Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser						
		500		505		510
Gly Gly Gly Gly Ser Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly						
		515		520		525
Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser						
		530		535		540
Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro						
		545		550		555
						560

Gly Lys Cys Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser
565 570 575

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
580 585 590

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
595 600 605

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser
610 615 620

Ala Trp Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
625 630 635 640

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
645 650 655

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
660 665 670

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
675 680 685

Ile Ser Ser Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
690 695 700

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
705 710 715 720

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
725 730 735

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr
740 745 750

Gly Tyr Leu His Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys Ser
755 760 765

<210> 143

<211> 2304

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polynucleotide construct

<400> 143

atggaagcac cagcgagct tctcttctc ctgctactct ggctcccaga taccaccgt

gaggtgcagc	tgttgagag	cgggggaggc	ttggtacagc	ctggggggtc	cctgcgcctc	120
tcctgtgcag	ccagcggatt	caccttttct	tacggttcta	tgtactgggt	ccgccaggct	180
ccaggggaagg	ggctggagt	ggtctcatct	atttcttctg	gttctgggtc	tacatactat	240
gcagactccg	tgaagggccg	gttcaccatc	tcccatgaca	attccaagaa	cacgctgtat	300
ctgcaaatga	acagcctgcg	tgccgaggac	acggctgtat	attattgtgc	gcgctcttct	360
tactacgggt	cttactactc	tattgactat	tggggccagg	gaaccctggg	caccgtctcc	420
tcaggtggag	gtggctccgg	gggtggagg	tccggaggag	gcggatcagg	tggaggcgga	480
agcgacatcc	agatgacca	gtctccatcc	tccctgagcg	catctgtagg	agaccgcgtc	540
accatcactt	gccgggcaag	tcagagcatt	agcagctatt	taaattggta	tcagcagaaa	600
ccagggaaag	cccctaagct	cctgatctat	gctgcattca	gtttgcaaag	tgggggtccca	660
tcacgtttca	gtggcagtgg	aagcgggaca	gatttcactc	tcaccatcag	cagtctacaa	720
cctgaagatt	ttgcaactta	ttactgtcaa	cagtactacg	acaacctgcc	cacttttggc	780
caggggacca	agctggagat	caaatcctcg	gagcccaa	cttctgacaa	aactcacaca	840
tgccaccgt	gccagcacc	tgaagccg	ggtgcaccgt	cagtcttcct	cttccccca	900
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gtgagccacg	aagacctga	ggtcaagttc	aactggtacg	tggacggcgt	ggaggtgcat	1020
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cagccggaga	acaactacaa	gaccacgcct	cccgtgctgg	actccgacgg	ctccttcttc	1380
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tccgtgatgc	atgaggctct	gcacaaccac	tacacgcaga	agagcctctc	cctgtctccg	1500
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ggaaagtgcc	tggagtgggt	gtccgctatc	tccggcagcg	gcggaagcac	ctactacgct	1740
gactccgtca	agggcagggt	caccatcagc	cgggacaaca	gcaagaacac	cctgtacctg	1800
cagatgaata	gcctcagggc	tgaagacacc	gctgtgtact	actgcgccag	gtactatggc	1860
ggctactact	ccgcctggat	ggactactgg	ggacagggca	cactggtgac	cgtgtccagc	1920
ggcggaggcg	gctccggagg	cggtggctcc	ggaggaggcg	gaagcggagg	aggaggctcc	1980

```

gatattcaga tgacacagtc ccctagctcc ctgtccgccg gcgtgggaga tcgggtgacc 2040
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ggaaaggctc ccaagctgct gatctacgcc gcttccagcc tccagagcgg cgtgcctagc 2160
aggttctccg gctccggaag cggaacagac ttcaccctga ccatcagctc cctgcagccc 2220
gaggacttcg ctacctacta ctgccagcag acctatggct acctgcacac cttcggctgc 2280
ggcacaaaagc tggagatcaa gcgc 2304

```

<210> 144

<211> 768

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polypeptide construct

<400> 144

```

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
1           5           10           15

```

```

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

```

```

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
          35           40           45

```

```

Phe Ser Tyr Gly Ser Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly
          50           55           60

```

```

Leu Glu Trp Val Ser Ser Ile Ser Ser Gly Ser Gly Ser Thr Tyr Tyr
65           70           75           80

```

```

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser His Asp Asn Ser Lys
          85           90           95

```

```

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
          100          105          110

```

```

Val Tyr Tyr Cys Ala Arg Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile
          115          120          125

```

```

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

```

```

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145          150          155          160

```

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 165 170 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
 180 185 190

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

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

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asp Asn Leu
 245 250 255

Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ser Ser Glu Pro
 260 265 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 275 280 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
 290 295 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 305 310 315 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
 325 330 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
 340 345 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
 355 360 365

Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro
 370 375 380

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
 385 390 395 400

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 405 410 415

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 420 425 430

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 435 440 445

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 450 455 460

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 465 470 475 480

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 485 490 495

Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 500 505 510

Gly Gly Gly Gly Ser Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly
 515 520 525

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 530 535 540

Gly Phe Asp Phe Glu Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro
 545 550 555 560

Gly Lys Cys Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser
 565 570 575

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 580 585 590

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
 595 600 605

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser
 610 615 620

Ala Trp Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 625 630 635 640

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
 645 650 655

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser

660

665

670

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
675 680 685

Ile Arg Ser Ala Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
690 695 700

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
705 710 715 720

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
725 730 735

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr
740 745 750

Gly Tyr Leu His Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys Arg
755 760 765

<210> 145

<211> 2304

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polynucleotide construct

<400> 145

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gaggtgcagc tgttgagag cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc	120
tcctgtgcag ccagcggatt caccttttct cacggttcta tgtactgggt ccgccaggct	180
ccaggggaagg ggctggagtg ggtctcatct atttcttctg gttctggttc tacatactat	240
gcagactccg tgaagggccg gttcaccatc tcccatgaca attccaagaa cacgctgtat	300
ctgcaaataga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct	360
tactacgggt cttactactc tattgactat tggggccagg gaaccctggt caccgtctcc	420
tcaggtggag gtggctccgg gggaggagg tccggaggag gcggatcagg tggaggcgga	480
agcgacatcc agatgacca gtctccatcc tccctgagcg catctgtagg agaccgcgtc	540
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa	600
ccagggaaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tgggggtcca	660
tcacgtttca gtggcagtgg aagcgggaca gatttcactc tcaccatcag cagtctacaa	720
cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc	780
caggggacca agctggagat caaatcgagt gagcccaaatt cttctgacaa aactcacaca	840

```

tgcccaccgt gccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttcccccca 900
aaaccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 960
gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat 1020
aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 1080
ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac 1140
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ccacaggtgt acaccctgcc cccatcccgg gatgagctga ccaagaacca ggtcagcctg 1260
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cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctcttcttc 1380
ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc 1440
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ggaaagtgcc tggagtgggt gtccgctatc tccggcagcg gcggaagcac ctactacgct 1740
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ggcggaggcg gctccggagg cggtagctcc ggaggaggcg gaagcggagg aggaggctcc 1980
gatattcaga tgacacagtc ccctagctcc ctgtccgcca gcgtgggaga tcgggtgacc 2040
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aggttctccg gctccggaag cggaacagac ttcaccctga ccatcagctc cctgcagccc 2220
gaggacttcg ctacctacta ctgccagcag acctatggct acctgcacac cttcggctgc 2280
ggcacaaagc tggagatcaa gcgc 2304

```

<210> 146

<211> 768

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polypeptide construct

<400> 146

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro

1	5	10	15
Asp Thr Thr Gly Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val	20	25	30
Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr	35	40	45
Phe Ser His Gly Ser Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly	50	55	60
Leu Glu Trp Val Ser Ser Ile Ser Ser Gly Ser Gly Ser Thr Tyr Tyr	65	70	75
Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser His Asp Asn Ser Lys	85	90	95
Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala	100	105	110
Val Tyr Tyr Cys Ala Arg Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile	115	120	125
Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly	130	135	140
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	145	150	155
Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val	165	170	175
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser	180	185	190
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu	195	200	205
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser	210	215	220
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln	225	230	235
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asp Asn Leu	245	250	255

Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Ser	Ser	Glu	Pro	260	265	270
Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	275	280	285
Ala	Ala	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	290	295	300
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	305	310	315
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	325	330	335
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	340	345	350
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	355	360	365
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Ala	Val	Ser	Asn	Lys	Ala	Leu	Pro	370	375	380
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	385	390	395
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	405	410	415
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	420	425	430
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	435	440	445
Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	450	455	460
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	465	470	475
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	485	490	495
Ser	Leu	Ser	Pro	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	500	505	510

Gly Gly Gly Gly Ser Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly
515 520 525

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
530 535 540

Gly Phe Asp Phe Glu Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro
545 550 555 560

Gly Lys Cys Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser
565 570 575

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
580 585 590

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
595 600 605

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser
610 615 620

Ala Trp Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
625 630 635 640

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
645 650 655

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
660 665 670

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
675 680 685

Ile Arg Ser Ala Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
690 695 700

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
705 710 715 720

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
725 730 735

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr
740 745 750

Gly Tyr Leu His Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys Arg
755 760 765

<210> 147
 <211> 2304
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polynucleotide construct

<400> 147

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tcctgtgcag ccagcggatt caccttttct cacggttcta tgtactgggt ccgccaggct	180
ccaggggaagg ggctggagtg ggtctcatct atttcttctg gttctggttc tacatactat	240
gcagactccg tgaagggccg gttcaccatc tcccatgaca attccaagaa cacgctgtat	300
ctgcaaatga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct	360
tactacgggt cttactactc tattgactat tggggccagg gaaccctggc caccgtctcc	420
tcaggtggag gtggctccgg gggaggaggt tccggaggag gcggatcagg tggaggcgga	480
agcgacatcc agatgaccca gtctccatcc tccctgagcg catctgtagg agaccgcgtc	540
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa	600
ccagggaaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tgggggtcca	660
tcacgtttca gtggcagtg aagcgggaca gatttcactc tcaccatcag cagtctacaa	720
cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc	780
caggggacca agctggagat caaatcgagt gagcccaaat cttctgacaa aactcacaca	840
tgcccaccgt gcccagcacc tgaagccgcg ggtgcaccgt cagtcttcct cttcccccca	900
aaaccaagg acaccctcat gatctccgg acccctgagg tcacatgcgt ggtggtggac	960
gtgagccacg aagaccctga ggtcaagttc aactggtacg tggacggcgt ggaggtgcat	1020
aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc	1080
ctcaccgtcc tgcaccagga ctggctgaat ggcaaggaat acaagtgcgc ggtctccaac	1140
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ccacaggtgt acaccctgcc cccatcccg gatgagctga ccaagaacca ggtcagcctg	1260
acctgcctgg tcaaaggctt ctatccaagc gacatcgccg tggagtggga gagcaatggg	1320
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctccttcttc	1380
ctctacagca agctcaccgt ggacaagagc aggtggcagc aggggaacgt cttctcatgc	1440
tccgtgatgc atgaggctct gcacaaccac tacacgcaga agagcctctc cctgtctccg	1500
ggttccggag gtggcggttc gggaggtggc gggtcaggag gtgggggatc cccttcagaa	1560

```

gtgcagctgc tggagtccgg aggaggactg gtgcagcctg gcggaagcct gaggctgagc      1620
tgcgctgcct ccggcttcga cttcgacagc tatgctatga gctgggtgag gcaagcccct      1680
ggaaagtgcc tggagtgggt gtccgctatc tccggcaggg gcggaagcac ctactacgct      1740
gactccgtca agggcaggtt caccatcagc cgggacaaca gcaagaacac cctgtacctg      1800
cagatgaata gcctcagggc tgaagacacc gctgtgtact actgcgccag gtactatggc      1860
ggctactact ccgcctggat ggactactgg ggacagggca cactggtgac cgtgtccagc      1920
ggcggaggcg gctccggagg cgggtggctcc ggaggaggcg gaagcggagg aggaggctcc      1980
gatattcaga tgacacagtc ccctagctcc ctgtccgccg gcgtgggaga tcgggtgacc      2040
atcacctgca gggccagcca gtccatcagg agcgccctga actggtacca gcagaagcct      2100
ggaaaggctc ccaagctgct gatctacgcc gcttcacagc tccagagcgg cgtgcctagc      2160
aggttctccg gctccggaag cggaacagac ttcaccctga ccatcagctc cctgcagccc      2220
gaggacttcg ctacctacta ctgccagcag acctatggct acctgcacac cttcggctgc      2280
ggcacaaagc tggagatcaa gcgc                                     2304

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<210> 148

<211> 768

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polypeptide construct

<400> 148

```

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1           5           10           15

```

```

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

```

```

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
35           40           45

```

```

Phe Ser His Gly Ser Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly
50           55           60

```

```

Leu Glu Trp Val Ser Ser Ile Ser Ser Gly Ser Gly Ser Thr Tyr Tyr
65           70           75           80

```

```

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser His Asp Asn Ser Lys
85           90           95

```

```

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
100          105          110

```

Val Tyr Tyr Cys Ala Arg Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile
115 120 125

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
165 170 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
180 185 190

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

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

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asp Asn Leu
245 250 255

Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ser Ser Glu Pro
260 265 270

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
275 280 285

Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
290 295 300

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
305 310 315 320

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
325 330 335

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
340 345 350

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp

355		360		365
Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro	370	375		380
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu	385	390	395	400
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn		405	410	415
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile		420	425	430
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr	435	440		445
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys	450	455	460	
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys	465	470	475	480
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu		485	490	495
Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser		500	505	510
Gly Gly Gly Gly Ser Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly	515		520	525
Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser	530	535		540
Gly Phe Asp Phe Asp Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro	545	550	555	560
Gly Lys Cys Leu Glu Trp Val Ser Ala Ile Ser Gly Arg Gly Gly Ser		565	570	575
Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp		580	585	590
Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu	595	600		605

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser
610 615 620

Ala Trp Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
625 630 635 640

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
645 650 655

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
660 665 670

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
675 680 685

Ile Arg Ser Ala Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
690 695 700

Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser
705 710 715 720

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
725 730 735

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr
740 745 750

Gly Tyr Leu His Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys Arg
755 760 765

<210> 149

<211> 2307

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polynucleotide construct

<400> 149

atggaagcac cagcgcagct tctcttctc ctgctactct ggctcccaga taccaccggt	60
gaggtgcagc tggttgagag cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc	120
tctgtgcag ccagcggatt caccttttct tacggttcta tgtactgggt ccgccaggct	180
ccaggggaagg ggctggagtg ggtctcatct atttcttctg gttctggttc tacatactat	240
gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat	300
ctgcaaatga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct	360
tactacggtt cttactactc tattgactat tggggccagg gaaccctggt caccgtctcc	420

tcaggcggcg gcggcagcgg cggcggcggc agcggcggcg gaggtccgg cggcggcggc	480
agcgacatcc agatgaccca gtctccatcc tccctgagcg catctgtagg agaccgcgtc	540
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa	600
ccagggaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tggggtccca	660
tcacgtttca gtggcagtgg aagcgggaca gatttcactc tcaccatcag cagtctgcaa	720
cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc	780
caggggacca agctggagat caaatcctcg agtgagccca aatcttctga caaaactcac	840
acatgccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc	900
ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg	960
gacgtgagcc acgaagaccc tgagggtcaag ttcaactggg acgtggacgg cgtggagggtg	1020
cataatgcc aagacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc	1080
gtcctcaccg tcctgcacca ggactggctg aatggcaagg aatacaagtg cgcggtctcc	1140
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga	1200
gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc	1260
ctgacctgcc tgggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat	1320
gggcagccgg agaacaacta caagaccacg cctcccgctg tggactccga cggtccttc	1380
ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca	1440
tgctccgtga tgcatgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct	1500
ccgggttccg gaggtggcgg ttccggagggt ggccgggtcag gaggtggggg atccccctca	1560
gaggtgcagc tgttgagag cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc	1620
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ctgcaaata gaagcctgcg tgccgaggac acggctgtat attattgtgc gcgtactac	1860
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tcaggcgggtg gaggcagcgg tgggggtggg tctggaggcg gtggcagtgg cggcggaggc	1980
tctgacatcc agatgaccca gtctccatcc tccctgagcg catctgtagg agaccgcgtc	2040
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa	2100
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tcacgtttca gtggcagtgg aagcgggaca gatttcactc tcaccatcag cagtctgcaa	2220
cctgaagatt ttgcaactta ttactgtcaa cagacttacg gttacctgca cacttttggc	2280
caggggacca agctggagat caaatca	2307

<210> 150
 <211> 769
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polypeptide construct

<400> 150

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Trp Leu Pro
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Asp Thr Thr Gly Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val
 20 25 30

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
 35 40 45

Phe Ser Tyr Gly Ser Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly
 50 55 60

Leu Glu Trp Val Ser Ser Ile Ser Ser Gly Ser Gly Ser Thr Tyr Tyr
 65 70 75 80

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
 85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 100 105 110

Val Tyr Tyr Cys Ala Arg Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile
 115 120 125

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 145 150 155 160

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 165 170 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
 180 185 190

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

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

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asp Asn Leu
 245 250 255

Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ser Ser Ser Glu
 260 265 270

Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 275 280 285

Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 290 295 300

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 305 310 315 320

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 325 330 335

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 340 345 350

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 355 360 365

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu
 370 375 380

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 385 390 395 400

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 420 425 430

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 435 440 445

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 450 455 460

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
465 470 475 480

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
485 490 495

Leu Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
500 505 510

Ser Gly Gly Gly Gly Ser Pro Ser Glu Val Gln Leu Leu Glu Ser Gly
515 520 525

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
530 535 540

Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala
545 550 555 560

Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly
565 570 575

Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
580 585 590

Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
595 600 605

Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Tyr Tyr
610 615 620

Ser Ala Trp Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
625 630 635 640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
660 665 670

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
675 680 685

Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
690 695 700

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

<400>	151						
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tcctgtgcag	ccagcggatt	caccttttct	tacggttcta	tgtactgggt	ccgccaggct		180
ccaggggaag	ggctggagtg	ggtctcatct	atttcttctg	gttctggttc	tacatactat		240
gcagactccg	tgaagggccg	gttcaccatc	tcccgtgaca	attccaagaa	cacgctgtat		300
ctgcaaata	acagcctgcg	tgccgaggac	acggctgtat	attattgtgc	gcgctcttct		360
tactacggtt	cttactactc	tattgactat	tggggccagg	gaaccctggt	caccgtctcc		420
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agcgacatcc	agatgacca	gtctccatcc	tccctgagcg	catctgtagg	agaccgcgtc		540
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ccagggaaag	cccctaagct	cctgatctat	gctgcatcca	gtttgcaaag	tggggtccca		660
tcacgtttca	gtggcagtg	aagcgggaca	gatttcactc	tcaccatcag	cagtctgcaa		720
cctgaagatt	ttgcaactta	ttactgtcaa	cagtactacg	acaacctgcc	cacttttggc		780
caggggacca	agctggagat	caaatcctcg	agtgagccca	aatcttctga	caaaactcac		840
acatgcccac	cgtgcccagc	acctgaagcc	gcgggtgcac	cgtcagttct	cctcttcccc		900
ccaaaaccca	aggacaccct	catgatctcc	cggacccctg	aggtcacatg	cgtggtggtg		960
gacgtgagcc	acgaagaccc	tgaggtcaag	ttcaactggt	acgtggacgg	cgtggaggtg		1020
cataatgcc	agacaaaagc	gcgggaggag	cagtacaaca	gcacgtaccg	tgtggtcagc		1080

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gtcctcaccg tcttgcacca ggactggctg aatggcaagg aatacaagtg cgcggtctcc 1140
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 1200
gaaccacagg tgtacaccct gcccccatcc cgggatgagc tgaccaagaa ccaggtcagc 1260
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agtggtggtg gcacatacta tgcagactcc gtgaagggcc gggtcaccat ctcccgtgac 2160
aattccaaga acacgtgtg tctgcaaag aacagcctgc gtgccgagga cacggctgta 2220
tattattgtg cgcgctacta cgggtggttac tactctgctt ggatggacta ttggggccag 2280
ggaaccctgg tcaccgtctc ctca 2304

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<210> 152

<211> 768

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polypeptide construct

<400> 152

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Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1           5           10           15

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

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Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr

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35		40		45											
Phe	Ser	Tyr	Gly	Ser	Met	Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly
50						55					60				
Leu	Glu	Trp	Val	Ser	Ser	Ile	Ser	Ser	Gly	Ser	Gly	Ser	Thr	Tyr	Tyr
65					70					75					80
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys
				85					90					95	
Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala
			100					105					110		
Val	Tyr	Tyr	Cys	Ala	Arg	Ser	Ser	Tyr	Tyr	Gly	Ser	Tyr	Tyr	Ser	Ile
		115					120					125			
Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly
	130					135					140				
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly
145					150					155					160
Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val
			165					170						175	
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser
			180					185					190		
Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu
	195						200					205			
Ile	Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser
	210					215					220				
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln
225					230					235					240
Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Tyr	Asp	Asn	Leu
			245					250						255	
Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Ser	Ser	Ser	Glu
			260					265					270		
Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro
	275						280					285			

Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 290 295 300

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 305 310 315 320

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 325 330 335

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 340 345 350

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 355 360 365

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu
 370 375 380

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 385 390 395 400

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 420 425 430

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 435 440 445

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 450 455 460

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 465 470 475 480

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 485 490 495

Leu Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 500 505 510

Ser Gly Gly Gly Gly Ser Pro Ser Asp Ile Gln Met Thr Gln Ser Pro
 515 520 525

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
 530 535 540

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
 545 550 555 560

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
 565 570 575

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 580 585 590

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
 595 600 605

Gln Gln Thr Tyr Gly Tyr Leu His Thr Phe Gly Gln Gly Thr Lys Leu
 610 615 620

Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 625 630 635 640

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly
 645 650 655

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
 660 665 670

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro
 675 680 685

Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser
 690 695 700

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
 705 710 715 720

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
 725 730 735

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser
 740 745 750

Ala Trp Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 755 760 765

<210> 153

<211> 2307

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polynucleotide construct

<400> 153

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tcctgtgcag ccagcggatt caccttttct tacggttcta tgtactgggt ccgccaggct	180
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gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat	300
ctgcaaatga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct	360
tactacggtt ctactactc tattgactat tggggccagg gaaccctgggt caccgtctcc	420
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cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc	780
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gacgtgagcc acgaagacc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg	1020
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc	1080
gtcctcaccg tcctgcacca ggactggctg aatggcaagg aatacaagtg cgcggtctcc	1140
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga	1200
gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc	1260
ctgacctgcc tgggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat	1320
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ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca	1440
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gaggtgcagc tgttgagag cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc	1620
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ccaggggaagt gcctggagt ggtctcagct attagtggta gtggtggtag cacatactat	1740
gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat	1800

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tctgacatcc agatgacca gtctccatcc tccctgagcg catctgtagg agaccgcgtc      2040
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa      2100
ccagggaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tgggggtccca      2160
tcacgtttca gtggcagtgg aagcgggaca gatttcactc tcaccatcag cagtctgcaa      2220
cctgaagatt ttgcaactta ttactgtcaa cagacttacg gttacctgca cacttttggc      2280
tgcgggacca agctggagat caaatca                                           2307

```

<210> 154

<211> 769

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polypeptide construct

<400> 154

```

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1           5           10           15

```

```

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

```

```

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
          35           40           45

```

```

Phe Ser Tyr Gly Ser Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly
          50           55           60

```

```

Leu Glu Trp Val Ser Ser Ile Ser Ser Gly Ser Gly Ser Thr Tyr Tyr
65           70           75           80

```

```

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
          85           90           95

```

```

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
          100          105          110

```

```

Val Tyr Tyr Cys Ala Arg Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile
          115          120          125

```

```

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

```

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
145 150 155 160

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
165 170 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
180 185 190

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

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

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asp Asn Leu
245 250 255

Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ser Ser Ser Glu
260 265 270

Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
275 280 285

Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
290 295 300

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
305 310 315 320

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
325 330 335

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
340 345 350

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
355 360 365

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu
370 375 380

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg

385		390		395		400
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys						
		405		410		415
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp						
		420		425		430
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys						
		435		440		445
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser						
		450		455		460
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser						
		465		470		475
						480
Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser						
		485		490		495
Leu Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly						
		500		505		510
Ser Gly Gly Gly Gly Ser Pro Ser Glu Val Gln Leu Leu Glu Ser Gly						
		515		520		525
Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala						
		530		535		540
Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala						
		545		550		555
						560
Pro Gly Lys Cys Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly						
		565		570		575
Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg						
		580		585		590
Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala						
		595		600		605
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Tyr Tyr						
		610		615		620
Ser Ala Trp Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser						
		625		630		635
						640

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
645 650 655

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
660 665 670

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
675 680 685

Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
690 695 700

Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro
705 710 715 720

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
725 730 735

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr
740 745 750

Tyr Gly Tyr Leu His Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys
755 760 765

Ser

<210> 155

<211> 2304

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polynucleotide construct

<400> 155

atggaagcac cagcgagct tctcttcctc ctgctactct ggctcccaga taccaccggt	60
gaggtgcagc tggtggagag cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc	120
tcctgtgcag ccagcggatt caccttttct tacggttcta tgtactgggt ccgccaggct	180
ccaggggaagg ggctggagtg ggtctcatct atttcttctg gttctggttc tacatactat	240
gcagactccg tgaagggccg gttcaccatc tcccgtgaca attccaagaa cacgctgtat	300
ctgcaaataa acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct	360
tactacgggtt cttactactc tattgactat tggggccagg gaaccctgggt caccgtctcc	420
tcaggcggcg gcggcagcgg cggcggcggc agcggcggcg gaggtccgg cggcggcggc	480
agcgacatcc agatgaccca gtctccatcc tccctgagcg catctgtagg agaccgcgtc	540

accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa	600
ccagggaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tggggtccca	660
tcacgtttca gtggcagtgg aagcgggaca gatttcactc tcaccatcag cagtctgcaa	720
cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc	780
caggggacca agctggagat caaatcctcg agtgagccca aatcttctga caaaactcac	840
acatgcccac cgtgcccagc acctgaagcc gcgggtgcac cgtcagtctt cctcttcccc	900
ccaaaaccca aggacaccct catgatctcc cggacccctg aggtcacatg cgtggtggtg	960
gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg	1020
cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc	1080
gtcctcaccg tcctgcacca ggactggctg aatggcaagg aatacaagtg cgcggtctcc	1140
aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga	1200
gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc	1260
ctgacctgcc tgggtcaaagg cttctatcca agcgacatcg ccgtggagtg ggagagcaat	1320
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggtccttc	1380
ttcctctaca gcaagctcac cgtggacaag agcaggtggc agcaggggaa cgtcttctca	1440
tgctccgtga tgcattgaggc tctgcacaac cactacacgc agaagagcct ctccctgtct	1500
ccgggttccg gaggtggcgg ttccggagggt ggccgggtcag gaggtggggg atccccctca	1560
gacatccaga tgaccagtc tccatcctcc ctgagcgcac ctgtaggaga ccgcgtcacc	1620
atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca	1680
gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca	1740
cgtttcagtg gcagtggaag cgggacagat ttcaactctca ccatcagcag tctgcaacct	1800
gaagattttg caacttatta ctgtcaacag acttacgggt acctgcacac ttttggtctgc	1860
gggaccaagc tggagatcaa aggcgggtgga ggcagcgggt ggggtgggtc tggaggcgggt	1920
ggcagtggcg gcggaggctc tgaggtgcag ctggtggaga gcgggggagg cttggtacag	1980
cctgggggggt ccctgcgcct ctctgtgca gccagcggat tcaccttag cagctatgcc	2040
atgagctggg tccgccaggc tccagggaag tgccctggagt gggctctcagc tattagtgggt	2100
agtggtggtg gcacatacta tgcagactcc gtgaagggcc ggttcacat ctcccgtagc	2160
aattccaaga acacgtgta tctgcaaatg aacagcctgc gtgccgagga cacggctgta	2220
tattattgtg cgcgctacta cgggtggttac tactctgctt ggatggacta ttggggccag	2280
ggaaccctgg tcaccgtctc ctca	2304

<210> 156

<211> 768

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polypeptide construct

<400> 156

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15

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

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
 35 40 45

Phe Ser Tyr Gly Ser Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly
 50 55 60

Leu Glu Trp Val Ser Ser Ile Ser Ser Gly Ser Gly Ser Thr Tyr Tyr
 65 70 75 80

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys
 85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 100 105 110

Val Tyr Tyr Cys Ala Arg Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile
 115 120 125

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 145 150 155 160

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 165 170 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
 180 185 190

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

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

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

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asp Asn Leu
 245 250 255

Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Ser Ser Ser Glu
 260 265 270

Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
 275 280 285

Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
 290 295 300

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
 305 310 315 320

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
 325 330 335

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
 340 345 350

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
 355 360 365

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu
 370 375 380

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
 385 390 395 400

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

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
 420 425 430

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 435 440 445

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 450 455 460

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 465 470 475 480

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
485 490 495

Leu Ser Leu Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
500 505 510

Ser Gly Gly Gly Gly Ser Pro Ser Asp Ile Gln Met Thr Gln Ser Pro
515 520 525

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
530 535 540

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
545 550 555 560

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
565 570 575

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
580 585 590

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
595 600 605

Gln Gln Thr Tyr Gly Tyr Leu His Thr Phe Gly Cys Gly Thr Lys Leu
610 615 620

Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
625 630 635 640

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly
645 650 655

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
660 665 670

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro
675 680 685

Gly Lys Cys Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser
690 695 700

Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
705 710 715 720

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu

725

730

735

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser
 740 745 750

Ala Trp Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 755 760 765

<210> 157
 <211> 699
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Made in Lab - antibody fragment

<400> 157
 tcgagtgagc ccaaattcttc tgacaaaact cacacatgcc caccgtgccc agcacctgaa 60
 gccgcgggtg caccgtcagt ctctctcttc cccccaaaac ccaaggacac cctcatgatac 120
 tcccggaacc ctgaggtcac atgcgtggtg gtggacgtga gccacgaaga ccctgaggtc 180
 aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag 240
 gagcagtaca acagcacgta ccgtgtggtc agcgtcctca ccgtcctgca ccaggactgg 300
 ctgaatggca aggaatacaa gtgcgcgggtc tccaacaaag ccctcccagc ccccatcgag 360
 aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca 420
 tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggcttctat 480
 ccaagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 540
 acgcctcccg tgctggactc cgacggctcc ttcttctctt acagcaagct caccgtggac 600
 aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 660
 aaccactaca cgcagaagag cctctccctg tctccgggt 699

<210> 158
 <211> 233
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Made in Lab - antibody fragment

<400> 158

Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys
 1 5 10 15

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

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
35 40 45

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
50 55 60

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
65 70 75 80

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
85 90 95

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn
100 105 110

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

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
130 135 140

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
145 150 155 160

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
165 170 175

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

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
195 200 205

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

Gln Lys Ser Leu Ser Leu Ser Pro Gly
225 230

<210> 159

<211> 693

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - antibody fragment

<400> 159

gagcccaaatt cttctgacaa aactcacaca tgcccaccgt gccagcacc tgaagccgcg

```

ggtgcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg      120
accctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc      180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      300
ggcaaggaat acaagtgcgc ggtctccaac aaagccctcc cagcccccat cgagaaaacc      360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccaagc      480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      540
cccgtgctgg actccgacgg ctcttcttct ctctacagca agctcaccgt ggacaagagc      600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      660
tacacgcaga agagcctctc cctgtctccg ggt                                     693

```

```

<210> 160
<211> 231
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Made in Lab - antibody fragment

```

```

<400> 160

```

```

Glu Pro Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1           5           10           15

```

```

Pro Glu Ala Ala Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20           25           30

```

```

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35           40           45

```

```

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50           55           60

```

```

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65           70           75           80

```

```

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85           90           95

```

```

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala
100          105          110

```

```

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

```

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

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

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly
 225 230

<210> 161
 <211> 768
 <212> DNA
 <213> Homo sapiens

<400> 161
 atgggaaaca gctgttacia catagtagcc actctgttgc tggtcctcaa ctttgagagg 60
 acaagatcat tgcaggatcc ttgtagtaac tgcccagctg gtacattctg tgataataac 120
 aggaatcaga tttgcagtcc ctgtcctcca aatagtttct ccagcgcagg tggacaaaagg 180
 acctgtgaca tatgcaggca gtgtaaagggt gttttcagga ccaggaagga gtgttcctcc 240
 accagcaatg cagagtgtga ctgcactcca gggtttcact gcctgggggc aggatgcagc 300
 atgtgtgaac aggattgtaa acaagggtcaa gaactgacaa aaaaagggtg taaagactgt 360
 tgctttggga catttaacga tcagaaacgt ggcactctgtc gaccctggac aaactgttct 420
 ttggatggaa agtctgtgct tgtgaatggg acgaaggaga gggacgtggt ctgtggacca 480
 tctccagccg acctctctcc gggagcatcc tctgtgaccc cgcctgcccc tgcgagagag 540
 ccaggacact ctccgcagat catctccttc tttcttgccg tgacgtcgac tgcgttgctc 600
 ttctgtctgt tcttcctcac gctccgtttc tctgttggtta aacggggcag aaagaaactc 660
 ctgtatatat tcaaacaacc atttatgaga ccagtacaaa ctactcaaga ggaagatggc 720
 tgtagctgcc gatttccaga agaagaagaa ggaggatgtg aactgtga 768

<210> 162
 <211> 255
 <212> PRT
 <213> Homo sapiens

<400> 162

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
 1 5 10 15

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
 20 25 30

Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
 35 40 45

Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
 50 55 60

Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
 65 70 75 80

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

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
 100 105 110

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
 115 120 125

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

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
 145 150 155 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
 165 170 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
 180 185 190

Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
 195 200 205

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
 210 215 220

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
 225 230 235 240

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
 245 250 255

<210> 163

<211> 1263

<212> DNA

<213> Homo sapiens

<400> 163

```

atgcctgggg ggtgctcccg gggccccgcc gccggggacg ggcgtctgcg gctggcgcgga      60
ctagcgctgg tactcctggg ctgggtctcc tcgtcttctc ccacctcctc ggcatcctcc      120
ttctcctcct cggcgcggtt cctggcttcc gccgtgtccg ccagagcccc gctgccggac      180
cagtgcctcc cgctgtgcca gtgctccgag gcagcgcgca cagtcaagtg cgtaaccgc      240
aatctgaccg aggtgcccac ggacctgccc gcctacgtgc gcaacctctt ccttaccggc      300
aaccagctgg ccgtgctccc tgccggcgcc ttgcgccgcc ggccgccgct ggccggagctg      360
gccgcgctca acctcagcgg cagccgcctg gacgaggtgc gcgcggggcg cttcgagcat      420
ctgcccagcc tgcgccagct cgacctcagc cacaaccacac tggccgacct cagtcccttc      480
gctttctcgg gcagcaatgc cagcgtctcg gccccagtc cccttgaggga actgatcctg      540
aaccacatcg tgccccctga agatgagcgg cagaaccgga gcttcgaggg catggtggtg      600
gcggccctgc tggcggggcg tgcaactgcag gggctccgcc gcttgagagct ggccagcaac      660
cacttccttt acctgccggg ggatgtgctg gcccaactgc ccagcctcag gcacctggac      720
ttaagtaata attcgctggg gagcctgacc tacgtgtcct tccgcaacct gacacatcta      780
gaaagcctcc acctggagga caatgccctc aaggctcctc acaatggcac cctggctgag      840
ttgcaaggtc taccacacat tagggttttc ctggacaaca atccctgggt ctgcgactgc      900
cacatggcag acatggtgac ctggctcaag gaaacagagg tagtgcaggg caaagaccgg      960
ctcacctgtg catatccgga aaaaatgagg aatcgggtcc tcttggaact caacagtgtc     1020
gacctggact gtgacctgat tcttccccca tccctgcaaa cctcttatgt cttcctgggt     1080
attgttttag ccctgatagg cgctattttc ctctgggttt tgtatttgaa ccgcaagggg     1140
ataaaaaagt ggatgcataa catcagagat gcctgcaggg atcacatgga agggatatcat     1200
tacagatatg aaatcaatgc ggacccccaga ttaacgaacc tcagttctaa ctcggatgtc     1260
tga                                                                    1263

```

<210> 164

<211> 420

<212> PRT

<213> Homo sapiens

<400> 164

Met Pro Gly Gly Cys Ser Arg Gly Pro Ala Ala Gly Asp Gly Arg Leu
1 5 10 15

Arg Leu Ala Arg Leu Ala Leu Val Leu Leu Gly Trp Val Ser Ser Ser
20 25 30

Ser Pro Thr Ser Ser Ala Ser Ser Phe Ser Ser Ser Ala Pro Phe Leu
35 40 45

Ala Ser Ala Val Ser Ala Gln Pro Pro Leu Pro Asp Gln Cys Pro Ala
50 55 60

Leu Cys Glu Cys Ser Glu Ala Ala Arg Thr Val Lys Cys Val Asn Arg
65 70 75 80

Asn Leu Thr Glu Val Pro Thr Asp Leu Pro Ala Tyr Val Arg Asn Leu
85 90 95

Phe Leu Thr Gly Asn Gln Leu Ala Val Leu Pro Ala Gly Ala Phe Ala
100 105 110

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

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

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

Ala Phe Ser Gly Ser Asn Ala Ser Val Ser Ala Pro Ser Pro Leu Val
165 170 175

Glu Leu Ile Leu Asn His Ile Val Pro Pro Glu Asp Glu Arg Gln Asn
180 185 190

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

Leu Gln Gly Leu Arg Arg Leu Glu Leu Ala Ser Asn His Phe Leu Tyr
210 215 220

Leu Pro Arg Asp Val Leu Ala Gln Leu Pro Ser Leu Arg His Leu Asp
225 230 235 240

Leu Ser Asn Asn Ser Leu Val Ser Leu Thr Tyr Val Ser Phe Arg Asn
245 250 255

Leu Thr His Leu Glu Ser Leu His Leu Glu Asp Asn Ala Leu Lys Val
260 265 270

Leu His Asn Gly Thr Leu Ala Glu Leu Gln Gly Leu Pro His Ile Arg
275 280 285

Val Phe Leu Asp Asn Asn Pro Trp Val Cys Asp Cys His Met Ala Asp
290 295 300

Met Val Thr Trp Leu Lys Glu Thr Glu Val Val Gln Gly Lys Asp Arg
305 310 315 320

Leu Thr Cys Ala Tyr Pro Glu Lys Met Arg Asn Arg Val Leu Leu Glu
325 330 335

Leu Asn Ser Ala Asp Leu Asp Cys Asp Pro Ile Leu Pro Pro Ser Leu
340 345 350

Gln Thr Ser Tyr Val Phe Leu Gly Ile Val Leu Ala Leu Ile Gly Ala
355 360 365

Ile Phe Leu Leu Val Leu Tyr Leu Asn Arg Lys Gly Ile Lys Lys Trp
370 375 380

Met His Asn Ile Arg Asp Ala Cys Arg Asp His Met Glu Gly Tyr His
385 390 395 400

Tyr Arg Tyr Glu Ile Asn Ala Asp Pro Arg Leu Thr Asn Leu Ser Ser
405 410 415

Asn Ser Asp Val
420

<210> 165

<211> 558

<212> DNA

<213> Homo sapiens

<400> 165

atgggaaaca gctgttaca catagtagcc actctgttgc tggctcctcaa ctttgagagg 60

acaagatcat tgcaggatcc ttgtagtaac tgcccagctg gtacattctg tgataataac 120

aggaatcaga tttgcagtcc ctgtcctcca aatagtttct ccagcgcagg tggacaaagg 180

acctgtgaca tatgcaggca gtgtaaagg gttttcagga ccaggaagga gtgttcctcc 240

accagcaatg cagagtgtga ctgcactcca gggtttcact gcctggggggc aggatgcagc 300

```

atgtgtgaac aggattgtaa acaaggtcaa gaactgacaa aaaaaggttg taaagactgt      360
tgctttggga catttaacga tcagaaacgt ggcattctgtc gaccttggaac aaactgttct      420
ttggatggaa agtctgtgct tgtgaatggg acgaaggaga gggacgtggg ctgtggacca      480
tctccagccg acctctctcc gggagcatcc tctgtgaccc cgcttgcccc tgcgagagag      540
ccaggacact ctccgcag                                         558

```

```

<210> 166
<211> 186
<212> PRT
<213> Homo sapiens

```

```

<400> 166

```

```

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
1           5           10           15

```

```

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
          20           25           30

```

```

Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
          35           40           45

```

```

Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
          50           55           60

```

```

Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
65           70           75           80

```

```

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

```

```

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
          100          105          110

```

```

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
          115          120          125

```

```

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

```

```

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
145           150           155           160

```

```

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
          165          170          175

```

Pro Ala Arg Glu Pro Gly His Ser Pro Gln
180 185

<210> 167
<211> 1065
<212> DNA
<213> Homo sapiens

<400> 167
atgcctgggg ggtgctcccg gggccccgcc gccggggacg ggcgtctgcg gctggcgcgga 60
ctagcgctgg tactcctggg ctgggtctcc tcgtcttctc ccacctctc ggcatacctcc 120
ttctcctcct cggcgcggtt cctggcttcc gccgtgtccg cccagcccc gctgccggac 180
cagtgccccg cgctgtgcga gtgctccgag gcagcgcgca cagtcaagtg cgttaaccgc 240
aatctgaccg aggtgcccac ggacctgcc gcctacgtgc gcaacctctt ccttaccggc 300
aaccagctgg ccgtgctccc tgccggcgcc ttccgccgcc ggccgccgct ggcggagctg 360
gccgcgctca acctcagcgg cagccgcctg gacgaggtgc gcgcggggcg cttcgagcat 420
ctgcccagcc tgcgccagct cgacctcagc cacaaccac tggccgacct cagtcccttc 480
gctttctcgg gcagcaatgc cagcgtctcg gccccagtc cccttggtga actgatcctg 540
aaccacatcg tgccccctga agatgagcgg cagaaccgga gcttcgaggg catggtggtg 600
gcggccctgc tggcgggccg tgcactgcag gggctccgcc gcttgagct ggccagcaac 660
cacttccttt acctgccg cgatgtgctg gcccaactgc ccagcctcag gcacctggac 720
ttaagtaata attcgctggt gagcctgacc tacgtgtcct tccgcaacct gacacatcta 780
gaaagcctcc acctggagga caatgccctc aaggtccttc acaatggcac cctggctgag 840
ttgcaaggtc taccacacat tagggttttc ctggacaaca atccctgggt ctgcgactgc 900
cacatggcag acatggtgac ctggctcaag gaaacagagg tagtgcaggg caaagaccgg 960
ctcacctgtg catatccgga aaaaatgagg aatcggggtcc tcttggaact caacagtgtc 1020
gacctggact gtgacctgat tcttccccca tccctgcaaa cctct 1065

<210> 168
<211> 355
<212> PRT
<213> Homo sapiens

<400> 168

Met Pro Gly Gly Cys Ser Arg Gly Pro Ala Ala Gly Asp Gly Arg Leu
1 5 10 15

Arg Leu Ala Arg Leu Ala Leu Val Leu Leu Gly Trp Val Ser Ser Ser
20 25 30

Ser Pro Thr Ser Ser Ala Ser Ser Phe Ser Ser Ser Ala Pro Phe Leu

35	40	45
Ala Ser Ala Val Ser Ala Gln Pro Pro Leu Pro Asp Gln Cys Pro Ala 50 55 60		
Leu Cys Glu Cys Ser Glu Ala Ala Arg Thr Val Lys Cys Val Asn Arg 65 70 75 80		
Asn Leu Thr Glu Val Pro Thr Asp Leu Pro Ala Tyr Val Arg Asn Leu 85 90 95		
Phe Leu Thr Gly Asn Gln Leu Ala Val Leu Pro Ala Gly Ala Phe Ala 100 105 110		
Arg Arg Pro Pro Leu Ala Glu Leu Ala Ala Leu Asn Leu Ser Gly Ser 115 120 125		
Arg Leu Asp Glu Val Arg Ala Gly Ala Phe Glu His Leu Pro Ser Leu 130 135 140		
Arg Gln Leu Asp Leu Ser His Asn Pro Leu Ala Asp Leu Ser Pro Phe 145 150 155 160		
Ala Phe Ser Gly Ser Asn Ala Ser Val Ser Ala Pro Ser Pro Leu Val 165 170 175		
Glu Leu Ile Leu Asn His Ile Val Pro Pro Glu Asp Glu Arg Gln Asn 180 185 190		
Arg Ser Phe Glu Gly Met Val Val Ala Ala Leu Leu Ala Gly Arg Ala 195 200 205		
Leu Gln Gly Leu Arg Arg Leu Glu Leu Ala Ser Asn His Phe Leu Tyr 210 215 220		
Leu Pro Arg Asp Val Leu Ala Gln Leu Pro Ser Leu Arg His Leu Asp 225 230 235 240		
Leu Ser Asn Asn Ser Leu Val Ser Leu Thr Tyr Val Ser Phe Arg Asn 245 250 255		
Leu Thr His Leu Glu Ser Leu His Leu Glu Asp Asn Ala Leu Lys Val 260 265 270		
Leu His Asn Gly Thr Leu Ala Glu Leu Gln Gly Leu Pro His Ile Arg 275 280 285		

Val Phe Leu Asp Asn Asn Pro Trp Val Cys Asp Cys His Met Ala Asp
 290 295 300

Met Val Thr Trp Leu Lys Glu Thr Glu Val Val Gln Gly Lys Asp Arg
 305 310 315 320

Leu Thr Cys Ala Tyr Pro Glu Lys Met Arg Asn Arg Val Leu Leu Glu
 325 330 335

Leu Asn Ser Ala Asp Leu Asp Cys Asp Pro Ile Leu Pro Pro Ser Leu
 340 345 350

Gln Thr Ser
 355

<210> 169
 <211> 744
 <212> DNA
 <213> ARTIFICIAL SEQUENCE

<220>
 <223> Made in Lab - Synthesized scFv sequence

<400> 169
 gacatccaga tgaccagtc tccatcctcc ctgagcgcac ctgtaggaga ccgcgtcacc 60
 atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120
 gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
 cgtttcagtg gcagtggaag cgggacagat ttactctca ccatcagcag tctgcaacct 240
 gaagattttg caacttatta ctgtcaacag acttacgggt acctgcacac ttttggccag 300
 gggaccaagc tggagatcaa aggcgggtgga ggcagcgggt ggggtgggtc tggaggcgggt 360
 ggcagtggcg gcggaggctc tgagggtgcag ctgttgaga gcgggggagg cttggtacag 420
 cctgggggggt ccctgcgcct ctctgtgca gccagcggat tcaccttag cagctatgcc 480
 atgagctggg tccgccaggc tccaggaag gggctggagt gggctctcagc tattagtgg 540
 agtggtggtg gcacatacta tgcagactcc gtgaagggcc gggtcaccat ctcccgtgac 600
 aattccaaga acacgtgta tctgcaaag aacagcctgc gtgccgagga cacggctgta 660
 tattattgtg cgcgctacta cggtggttac tactctgctt ggatggacta ttggggccag 720
 ggaaccctgg tcaccgtctc ctca 744

<210> 170
 <211> 248
 <212> PRT
 <213> ARTIFICIAL SEQUENCE

<220>
 <223> Made in Lab - Synthesized scFv sequence

<400> 170

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

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

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

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

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr Leu His
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
 100 105 110

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

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

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala
 145 150 155 160

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

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

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

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 210 215 220

Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp Met Asp Tyr Trp Gly Gln
 225 230 235 240

Gly Thr Leu Val Thr Val Ser Ser
245

<210> 171
<211> 2298
<212> DNA
<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polynucleotide construct

<400> 171
atggaagcac cagcgcagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60
gaggtgcagc tgttgagag cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc 120
tcctgtgcag ccagcggatt caccttttct cacggttcta tgtactgggt ccgccaggct 180
ccaggggaagg ggctggagt ggtctcatct atttcttctg gttctggttc tacatactat 240
gcagactccg tgaagggccg gttcaccatc tcccatgaca attccaagaa cacgctgtat 300
ctgcaaatga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct 360
tactacggtt cttactactc tattgactat tggggccagg gaaccctggc caccgtctcc 420
tcaggtggag gtggctccgg ggggtggagg tccggaggag gcggatcagg tggaggcgga 480
agcgacatcc agatgacca gtctccatcc tccctgagcg catctgtagg agaccgcgtc 540
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa 600
ccagggaaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tgggggtcca 660
tcacgtttca gtggcagtgg aagcgggaca gatttcactc tcaccatcag cagtctacaa 720
cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc 780
caggggacca agctggagat caaagagccc aaatcttctg acaaaactca cacatgcccc 840
ccgtgcccag cacctgaagc cgggggtgca ccgtcagtct tcctcttccc cccaaaaccc 900
aaggacaccc tcatgatctc ccggacccct gaggtcacat gcgtgggtgg ggacgtgagc 960
cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggagggt gcataatgcc 1020
aagacaaagc cgggggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 1080
gtcctgcacc aggactggct gaatggcaag gaatacaagt gcgcgggtct caacaaagcc 1140
ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag 1200
gtgtacaccc tgccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 1260
ctgggtcaaag gcttctatcc aagcgacatc gccgtggagt gggagagcaa tgggcagccg 1320
gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 1380
agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 1440
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggttcc 1500

```

ggaggtggcg gttcgggagg tggcgggtca ggaggtgggg gatccccttc agaagtgcag      1560
ctgctggagt ccgaggagg actggtgcag cctggcgga gcctgaggct gagctgcgct      1620
gcctccggct tcacattcag cagctatgct atgagctggg tgaggcaagc ccctggaaag      1680
ggcctggagt ggggtgtccgc tatctccggc agcggcgga gcacctacta cgctgactcc      1740
gtcaagggca ggttcaccat cagccgggac aacagcaaga acaccctgta cctgcagatg      1800
aatagcctca gggctgaaga caccgctgtg tactactgcg ccaggctacta tggcggctac      1860
tactccgcct ggatggacta ctggggacag ggcacactgg tgaccgtgtc cagcggcgga      1920
ggcggctccg gaggcgggtg ctccggagga ggcggaagcg gaggaggagg ctccgatatt      1980
cagatgacac agtcccctag ctccctgtcc gccagcgtgg gagatcgggt gaccatcacc      2040
tgcagggcca gccagtccat ctccagcttc ttaaactggg accagcagaa gcctggaaag      2100
gctccaagc tgctgatcta cgccgcttcc agcctccaga gcggcgtgcc tagcaggttc      2160
tccggctccg gaagcggaac agacttcacc ctgaccatca gctccctgca gcccaggac      2220
tccgtacct actactgcca gcagacctat ggctacctgc acaccttcgg ccagggcaca      2280
aagctggaga tcaagcgc      2298

```

<210> 172

<211> 766

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polypeptide construct

<400> 172

```

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1           5           10           15

```

```

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

```

```

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
35           40           45

```

```

Phe Ser His Gly Ser Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly
50           55           60

```

```

Leu Glu Trp Val Ser Ser Ile Ser Ser Gly Ser Gly Ser Thr Tyr Tyr
65           70           75           80

```

```

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser His Asp Asn Ser Lys
85           90           95

```

Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala			
			100					105					110					
Val	Tyr	Tyr	Cys	Ala	Arg	Ser	Ser	Tyr	Tyr	Gly	Ser	Tyr	Tyr	Ser	Ile			
		115					120					125						
Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly			
	130					135					140							
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly			
145					150					155					160			
Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val			
			165					170						175				
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser			
			180					185					190					
Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu			
		195					200					205						
Ile	Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser			
	210					215					220							
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln			
225					230					235					240			
Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Tyr	Asp	Asn	Leu			
			245					250						255				
Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Glu	Pro	Lys	Ser			
		260					265						270					
Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala			
		275				280					285							
Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu			
	290					295				300								
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser			
305					310					315					320			
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu			
			325					330					335					
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr			
		340					345						350					

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365

Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 405 410 415

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 450 455 460

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495

Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 500 505 510

Gly Gly Ser Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
 515 520 525

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 530 535 540

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 545 550 555 560

Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
 565 570 575

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 580 585 590

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 595 600 605

Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp
610 615 620

Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
625 630 635 640

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
645 650 655

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
660 665 670

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
675 680 685

Ser Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
690 695 700

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
705 710 715 720

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
725 730 735

Gln Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr
740 745 750

Leu His Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
755 760 765

<210> 173

<211> 2298

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polynucleotide construct

<400> 173

atggaagcac cagcgagct tctcttcctc ctgctactct ggctcccaga taccaccggt 60

gaggtgcagc tggtggagag cgggggaggc ttggtacagc ctgggggggtc cctgcgcctc 120

tcctgtgcag ccagcggatt caccttttct cacggttcta tgtactgggt ccgccaggct 180

ccaggggaagg ggctggagtg ggtctcatct atttcttctg gttctggttc tacatactat 240

gcagactccg tgaagggccg gttcaccatc tcccatgaca attccaagaa cacgctgtat 300

ctgcaaatga acagcctgcg tgccgaggac acggctgtat attattgtgc gcgctcttct 360

tactacggtt	cttactactc	tattgactat	tggggccagg	gaaccctggt	caccgtctcc	420
tcaggtggag	gtggctccgg	gggtggaggt	tccggaggag	gcggatcagg	tggaggcgga	480
agcgacatcc	agatgacca	gtctccatcc	tccctgagcg	catctgtagg	agaccgcgtc	540
accatcactt	gccgggcaag	tcagagcatt	agcagctatt	taaattggta	tcagcagaaa	600
ccagggaaag	cccctaagct	cctgatctat	gctgcatcca	gtttgcaaag	tgggggtcca	660
tcacgtttca	gtggcagtgg	aagcgggaca	gatttcactc	tcaccatcag	cagtctacaa	720
cctgaagatt	ttgcaactta	ttactgtcaa	cagtactacg	acaacctgcc	cacttttggc	780
caggggacca	agctggagat	caaagagccc	aaatcttctg	acaaaactca	cacatgcca	840
ccgtgcccag	cacctgaagc	cgcggttgca	ccgtcagttc	tcctcttccc	cccaaaaccc	900
aaggacaccc	tcatgatctc	ccggacccct	gaggtcacat	gcgtgggtgt	ggacgtgagc	960
cacgaagacc	ctgaggtcaa	gttcaactgg	tacgtggacg	gcgtggaggt	gcataatgcc	1020
aagacaaagc	cgcgggagga	gcagtacaac	agcacgtacc	gtgtgggtcag	cgtcctcacc	1080
gtcctgcacc	aggactggct	gaatggcaag	gaatacaagt	gcgcggtctc	caacaaagcc	1140
ctcccagccc	ccatcgagaa	aaccatctcc	aaagccaaag	ggcagccccg	agaaccacag	1200
gtgtacaccc	tgccccatc	ccgggatgag	ctgaccaaga	accaggtcag	cctgacctgc	1260
ctggtcaaag	gcttctatcc	aagcgacatc	gccgtggagt	gggagagcaa	tgggcagccg	1320
gagaacaact	acaagaccac	gcctcccgtg	ctggactccg	acggctcctt	cttcctctac	1380
agcaagctca	ccgtggacaa	gagcaggtgg	cagcagggga	acgtcttctc	atgctccgtg	1440
atgcatgagg	ctctgcacaa	ccactacacg	cagaagagcc	tctccctgtc	tccgggttcc	1500
ggaggtggcg	gttcgggagg	tggcgggtca	ggaggtgggg	gatccccttc	agaagtgcag	1560
ctgctggagt	ccggaggagg	actggtgcag	cctggcgga	gcctgaggct	gagctgcgct	1620
gcctccggct	tcacattcag	cagctatgct	atgagctggg	tgaggcaagc	ccctggaaag	1680
tgcttgagg	gggtgtccgc	tatctccggc	agcggcgga	gcacctacta	cgctgactcc	1740
gtcaagggca	ggttcaccat	cagccgggac	aacagcaaga	acaccctgta	cctgcagatg	1800
aatagcctca	gggctgaaga	caccgctgtg	tactactgcg	ccaggtacta	tggcggctac	1860
tactccgcct	ggatggacta	ctggggacag	ggcacactgg	tgaccgtgtc	cagcggcgga	1920
ggcggctccg	gaggcggtgg	ctccggagga	ggcggaagcg	gaggaggagg	ctccgatatt	1980
cagatgacac	agtcccctag	ctccctgtcc	gccagcgtgg	gagatcgggt	gaccatcacc	2040
tgcaaggcca	gccagtccat	ctccagcttc	ttaaactggg	accagcagaa	gcctggaaag	2100
gctcccaagc	tgctgatcta	cgccgcttcc	agcctccaga	gcggcgtgcc	tagcaggttc	2160
tccggctccg	gaagcggaac	agacttcacc	ctgaccatca	gctccctgca	gcccgaggac	2220
tccgctacct	actactgcca	gcagacctat	ggctacctgc	acaccttcgg	ctgcggcaca	2280

aagctggaga tcaagcgc

2298

<210> 174

<211> 766

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polypeptide construct

<400> 174

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
 1 5 10 15

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

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
 35 40 45

Phe Ser His Gly Ser Met Tyr Trp Val Arg Gln Ala Pro Gly Lys Gly
 50 55 60

Leu Glu Trp Val Ser Ser Ile Ser Ser Gly Ser Gly Ser Thr Tyr Tyr
 65 70 75 80

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser His Asp Asn Ser Lys
 85 90 95

Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala
 100 105 110

Val Tyr Tyr Cys Ala Arg Ser Ser Tyr Tyr Gly Ser Tyr Tyr Ser Ile
 115 120 125

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

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 145 150 155 160

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 165 170 175

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser
 180 185 190

Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu

195		200		205
Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser				
210		215		220
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln				
225		230		235 240
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Asp Asn Leu				
		245		250 255
Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Glu Pro Lys Ser				
		260		265 270
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala				
		275		280 285
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu				
		290		295 300
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser				
305		310		315 320
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu				
		325		330 335
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr				
		340		345 350
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn				
		355		360 365
Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro				
		370		375 380
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln				
385		390		395 400
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val				
		405		410 415
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val				
		420		425 430
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro				
		435		440 445

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 450 455 460

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495

Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 500 505 510

Gly Gly Ser Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
 515 520 525

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
 530 535 540

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 545 550 555 560

Cys Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr
 565 570 575

Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
 580 585 590

Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr
 595 600 605

Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp
 610 615 620

Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
 625 630 635 640

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
 645 650 655

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
 660 665 670

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
 675 680 685

Ser Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
 690 695 700

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
705 710 715 720

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
725 730 735

Gln Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr
740 745 750

Leu His Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys Arg
755 760 765

<210> 175

<211> 2298

<212> DNA

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polynucleotide construct

<400> 175

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atggaagcac cagcgcagct tctcttctc ctgctactct ggctcccaga taccaccggt      60
gaggtgcagc tggttgagag cgggggagggc ttggtacagc ctgggggggtc cctgcgcctc      120
tctgtgcag ccagcggatt caccttttct cacggttcta tgtactgggt ccgccaggct      180
ccaggggaagg ggctggagtg ggtctcatct atttcttctg gttctggttc tacatactat      240
gcagactccg tgaagggccg gttcaccatc tcccatgaca attccaagaa cacgctgtat      300
ctgcaaatga acagcctgcg tgccgaggac acggtgtat attattgtgc gcgctcttct      360
tactacggtt ctactactc tattgactat tggggccagg gaaccctggc caccgtctcc      420
tcaggtggag gtggctccgg gggaggaggt tccggaggag gcggatcagg tggaggcgga      480
agcgacatcc agatgacca gtctccatcc tccctgagcg catctgtagg agaccgcgtc      540
accatcactt gccgggcaag tcagagcatt agcagctatt taaattggta tcagcagaaa      600
ccagggaaag cccctaagct cctgatctat gctgcatcca gtttgcaaag tgggggtcca      660
tcacgtttca gtggcagtgg aagcgggaca gatttcactc tcaccatcag cagtctacaa      720
cctgaagatt ttgcaactta ttactgtcaa cagtactacg acaacctgcc cacttttggc      780
caggggacca agctggagat caaagagccc aaatcttctg acaaaactca cacatgcccc      840
ccgtgcccag cacctgaagc cgcgggtgca ccgtcagtct tcctcttccc cccaaaaccc      900
aaggacaccc tcatgatctc ccggaccctt gaggtcacat gcgtgggtgg ggacgtgagc      960
cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc      1020
aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc      1080
gtcctgcacc aggactggct gaatggcaag gaatacaagt gcgcgggtct caacaaagcc      1140

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ctcccagccc ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agaaccacag      1200
gtgtacaccc tgcccccatc ccgggatgag ctgaccaaga accagggtcag cctgacctgc      1260
ctgggtcaaag gcttctatcc aagcgacatc gccgtggagt gggagagcaa tgggcagccg      1320
gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac      1380
agcaagctca ccgtggacaa gagcagggtg cagcagggga acgtcttctc atgctccgtg      1440
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggttcc      1500
ggagggtggcg gttcgggagg tggcgggtca ggagggtggg gatccccttc agaagtgcag      1560
ctgctggagt ccggaggagg actggtgcag cctggcgga gcctgaggct gagctgcgct      1620
gcctccggct tcacattcag cagctatgct atgagctggg tgaggcaagc ccctggaaag      1680
ggcctggagt ggggtgtccgc tatctccggc agcggcgga gcacctacta cgctgactcc      1740
gtcaagggca ggttcaccat cagccgggac aacagcaaga acaccctgta cctgcagatg      1800
aatagcctca gggctgaaga caccgctgtg tactactgcg ccaggacta tggcggctac      1860
tactccgcct ggatggacta ctggggacag ggcacactgg tgaccgtgtc cagcggcgga      1920
ggcggctccg gaggcggtgg ctccggagga ggcggaagcg gaggaggagg ctccgatatt      1980
cagatgacac agtcccctag ctccctgtcc gccagcgtgg gagatcgggt gaccatcacc      2040
tgcagggcca gccagtccat ctccagctat ttaaactggg accagcagaa gcctggaaag      2100
gctcccaagc tgctgatcta cgccgcttcc agcctccaga gcggcgtgcc tagcaggttc      2160
tccggctccg gaagcggaac agacttcacc ctgaccatca gctccctgca gcccaggac      2220
tccgtacct actactgcca gcagacctat ggctacctgc acaccttcgg ccagggcaca      2280
aagctggaga tcaagcgc                                     2298

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<210> 176

<211> 766

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in Lab - anti-5T4 x anti-4-1BB polypeptide construct

<400> 176

```

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1           5           10           15

```

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

```

```

Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
35           40           45

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Phe	Ser	His	Gly	Ser	Met	Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly		
50						55					60						
Leu	Glu	Trp	Val	Ser	Ser	Ile	Ser	Ser	Gly	Ser	Gly	Ser	Thr	Tyr	Tyr		
65				70					75						80		
Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	His	Asp	Asn	Ser	Lys		
				85					90					95			
Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala		
		100						105					110				
Val	Tyr	Tyr	Cys	Ala	Arg	Ser	Ser	Tyr	Tyr	Gly	Ser	Tyr	Tyr	Ser	Ile		
		115					120					125					
Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly		
	130					135					140						
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly		
145					150					155					160		
Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val		
				165					170					175			
Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Gln	Ser	Ile	Ser	Ser		
			180					185					190				
Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu		
		195					200					205					
Ile	Tyr	Ala	Ala	Ser	Ser	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser		
	210					215					220						
Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln		
225					230					235					240		
Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Tyr	Asp	Asn	Leu		
				245					250					255			
Pro	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Glu	Pro	Lys	Ser		
			260					265					270				
Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Ala		
		275					280					285					
Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu		
	290					295					300						

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
305 310 315 320

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
325 330 335

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
340 345 350

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
355 360 365

Gly Lys Glu Tyr Lys Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
370 375 380

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
385 390 395 400

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
405 410 415

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
420 425 430

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
435 440 445

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
450 455 460

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
465 470 475 480

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
485 490 495

Ser Pro Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
500 505 510

Gly Gly Ser Pro Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu
515 520 525

Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe
530 535 540

Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys

545		550		555		560
Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr						
		565		570		575
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser						
		580		585		590
Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr						
		595		600		605
Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Tyr Tyr Ser Ala Trp						
		610		615		620
Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly						
		625		630		635
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly						
		645		650		655
Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser						
		660		665		670
Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser						
		675		680		685
Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu						
		690		695		700
Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe						
		705		710		715
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu						
		725		730		735
Gln Pro Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Gly Tyr						
		740		745		750
Leu His Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg						
		755		760		765

<210> 177

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> ACN017 CDRH1 Sequence

<400> 177

Ala Lys Gly Ser Gly Ser Tyr Phe Asp Leu
 1 5 10

<210> 178

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> ACN017 CDRL3

<400> 178

Gln Gln Tyr Ser Gly Tyr Pro Tyr Thr
 1 5

<210> 179

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> ACN017 VH

<400> 179

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

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

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

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

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

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

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

Val Thr Val Ser Ser
 115

<210> 180

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

<220>
 <223> ACN017 VL

<400> 180

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

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

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

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

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

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

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

<210> 181
 <211> 741
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> ACN017 Full

<400> 181

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

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

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

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

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

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

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

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

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

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

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

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

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

Leu Glu Ile Lys Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr
 245 250 255

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Ala Pro Ser Val Phe
 260 265 270

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
 275 280 285

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
 290 295 300

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
 305 310 315 320

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

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 340 345 350

Ala Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 355 360 365

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 370 375 380

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 385 390 395 400

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 405 410 415

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 420 425 430

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 435 440 445

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 450 455 460

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Ser Gly Gly
 465 470 475 480

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Pro Ser Glu
 485 490 495

Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
 500 505 510

Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala
 515 520 525

Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
 530 535 540

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
 545 550 555 560

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
 565 570 575

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
580 585 590

Lys Gly Ser Gly Ser Tyr Phe Asp Leu Trp Gly Gln Gly Thr Leu Val
595 600 605

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
610 615 620

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
625 630 635 640

Ser Phe Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
645 650 655

Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
660 665 670

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser
675 680 685

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
690 695 700

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
705 710 715 720

Gln Gln Tyr Ser Gly Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu
725 730 735

Glu Ile Lys Arg Ser
740